

Fig. 1A

	10	20	30	40	50	60
BTHKURHD	ATGGATAACAATCCGAACATCAATGAATGCATTCCCTTATAATTGTTTAAGTAACCCTGAA					
flsynbt.fin	...C...C...C...C...G...C...C...C...CC.G...C...C...G					
bssyn	...C...C...C...C...G...C...C...C...CC.G...C...C...G					
	70	80	90	100	110	120
BTHKURHD	GTAGAAGTATTAGGTGGAGAAAGAATAGAACTGGTTACACCCCAATCGATATTCCTTG					
flsynbt.fin	..G..G..GC.G..C..C..GC.C..C..G..C..C.....C.....C..CAG.C..					
bssyn	..G..G..GC.G..C..C..GC.C..C..G..C..C.....C.....C..CAG.C..					
	130	140	150	160	170	180
BTHKURHD	TCGCTAACGCAATTTCTTTTGTAGTGAATTTGTTCCCGGTGCTGGATTTGTGTAGGACTA					
flsynbt.fin	AGC..G..C..G..C..GC..C..G..C..G.....C..C..C..C..C..G..C..G					
bssyn	AGC..G..C..G..C..GC..C..G..C..G.....C..C..C..C..C..G..C..G					
	190	200	210	220	230	240
BTHKURHD	GTTGATATAATATGGGGAATTTTGTGTCCTCTCAATGGGACGCATTTCTTGTACAAATT					
flsynbt.fin	..G..C..C..C.....C..C..C..C..AGC..G.....C..C..G..G..G..C					
bssyn	..G..C..C..C.....C..C..C..C..AGC..G.....C..C..G..G..G..C					
	250	260	270	280	290	300
BTHKURHD	GAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA					
flsynbt.fin	..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G					
bssyn	..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G					
	310	320	330	340	350	360
BTHKURHD	GAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGAT					
flsynbt.fin	..G..C..G.....C..G..C.....C.....C..GAGC..CC.C.....G..C..C					
bssyn	..G..C..G.....C..G..C.....C.....C..GAGC..CC.C.....G..C..C					
	370	380	390	400	410	420
BTHKURHD	CCTACTAATCCAGCATTAAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCC					
flsynbt.fin	..C..C..C..C..CC.GC.C..G.....C..C..G.....C.....C...					
bssyn	..C..C..C..C..CC.GC.C..G.....C..C..G.....C.....C...					
	430	440	450	460	470	480
BTHKURHD	CTTACAACCGCTATTCTCTTTTGCAGTTCAAAATTATCAAGTTCCTCTTTTATCAGTA					
flsynbt.fin	..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G					
bssyn	..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G					
	490	500	510	520	530	540
BTHKURHD	TATGTTCAAGCTGCAAATTTACATTTATCAGTTTTGAGAGATGTTTCAGTGTGGACAA					
flsynbt.fin	..C..G..G..C..C..CC.G..CC.GAGC..GC..C..C..C..CAGC.....C..C..G					
bssyn	..C..G..G..C..C..CC.G..CC.GAGC..GC..C..C..C..CAGC.....C..C..G					
	550	560	570	580	590	600
BTHKURHD	AGGTGGGGATTGATGCCGCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTATT					
flsynbt.fin	C.C.....C..C..C.....C..C.....C..C..C..C..CC.G..CC.C..G..C					
bssyn	C.C.....C..C..C.....C..C.....C..C..C..C..CC.G..CC.C..G..C					

099842-112001

Fig. 1B

BTHKURHD
 flsynbt.fin
 bssyn

610* 620* 630* 640* 650* 660*
 GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA
C..C..C..C..C..G.....C..C..CC.G.....C..G.....T
C..C..C..C..C..G.....C..C..CC.G.....C..G.....T

BTHKURHD
 flsynbt.fin
 bssyn

670* 680* 690* 700* 710* 720*
 CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAAGTGT
 ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G
 ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G

BTHKURHD
 flsynbt.fin
 bssyn

730* 740* 750* 760* 770* 780*
 TTAGATATCGTTTCTCTATTTCGGAATATGATAGTAGAACGTATCCAATTGGAACAGTT
 C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..G
 C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..G

BTHKURHD
 flsynbt.fin
 bssyn

790* 800* 810* 820* 830* 840*
 TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTTT
 AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C
 AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C

BTHKURHD
 flsynbt.fin
 bssyn

850* 860* 870* 880* 890* 900*
 CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT
 ..C...AGC..C.....C..G..C..C..CC.C..C..C..CC.....C..C..G
 ..C...AGC..C.....C..G..C..C..CC.C..C..C..CC.....C..C..G

BTHKURHD
 flsynbt.fin
 bssyn

910* 920* 930* 940* 950* 960*
 AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA
C..C.....C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G
C..C.....C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G

BTHKURHD
 flsynbt.fin
 bssyn

970* 980* 990* 1000* 1010* 1020*
 ATAATGGCTTCTCCTGTAGGGTTTTTCGGGGCCAGAATTCACCTTTCCGCTATATGGAAGT
 ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C
 ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C

BTHKURHD
 flsynbt.fin
 bssyn

1030* 1040* 1050* 1060* 1070* 1080*
 ATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGA
C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C
C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C

BTHKURHD
 flsynbt.fin
 bssyn

1090* 1100* 1110* 1120* 1130* 1140*
 ACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACCTA
 ..CC.GAGCAG...CC.G..CC.TC.....C..C..C..C..C..C..G..G..G
 ..CC.GAGCAG...CC.G..CC.TC.....C..C..C..C..C..C..G..G..G

BTHKURHD
 flsynbt.fin
 bssyn

1150* 1160* 1170* 1180* 1190* 1200*
 TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA
 AGC..G..G.....C..C..G..C..C..C..C..AG.AGC..CC....CAG...C..G
 AGC..G..G.....C..C..G..C..C..C..C..AG.AGC..CC....CAG...C..G

09988462-12001

Fig. 1C

	1210*	1220*	1230*	1240*	1250*	1260*
BTHKURHD	TACAGAAAAAGCGGAACGGTAGATTTCGCTGGATGAAATACCGCCACAGAATAACAACGTG					
flsynbt.fin	...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.....					
bssyn	...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.....					
	1270*	1280*	1290*	1300*	1310*	1320*
BTHKURHD	CCACCTAGGCAAGGATTTAGTCATCGATTAAAGCCATGTTTCAATGTTTCGTTTCAGGCTTT					
flsynbt.finC.A..G..C..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C					
bssynC.A..G..C..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C					
	1330*	1340*	1350*	1360*	1370*	1380*
BTHKURHD	AGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCT					
flsynbt.fin	..C..C..C..C..G..C..C..CC.T..A.....AGC.....T..C..C.....C					
bssyn	..C..C..C..C..G..C..C..CC.T..A.....AGC.....T..C..C.....C					
	1390*	1400*	1410*	1420*	1430*	
BTHKURHD	GAATTTAATAATATAATTTCCTTCATCA--CAAATTACACAAATACCTTTAACAAAATCTA					
flsynbt.fin	..G..C..C..C..C..C..C.--..G..GC..G..C..C..G..C..CC.G..C..GAGC.					
bssyn	..G..C..C..C..C..C..C.--..G..GC..G..C..C..G..C..CC.G..C..GAGC.					
	1440*	1450*	1460*	1470*	1480*	1490*
BTHKURHD	CTAATCTTGGCTCTGGAACCTTCTGTCGTTAAAGGACCAGGATTTACAGGAGGAGATATTC					
flsynbt.fin	.C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C..C					
bssyn	.C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C..C					
	1500*	1510*	1520*	1530*	1540*	1550*
BTHKURHD	TTCGAAGAACTTCACCTGGCCAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT					
flsynbt.fin	.G..CC.C..CAGC..C.....CAGC...C.GC.C..G..C..C..C..C..CC.GA					
bssyn	.G..CC.C..CAGC..C.....CAGC...C.GC.C..G..C..C..C..C..CC.GA					
	1560*	1570*	1580*	1590*	1600*	1610*
BTHKURHD	CACAAAGATATCGGGTAAGAATTTCGCTACGCTTCTACCACAAATTTACAATTCCATACAT					
flsynbt.fin	GC..GC.C..C..C..CC.C..C.....CAGC.....C..CC.G..G.....C..CA					
bssyn	GC..GC.C..C..C..CC.C..C.....CAGC.....C..CC.G..G.....C..CA					
	1620*	1630*	1640*	1650*	1660*	1670*
BTHKURHD	CAATTGACGGAAGACCTATTAATCAGGGGAATTTTTTCAGCAACTATGAGTAGTGGGAGTA					
flsynbt.fin	GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C					
bssyn	GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C					
	1680*	1690*	1700*	1710*	1720*	1730*
BTHKURHD	ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTTACTACTCCGTTTAACTTTTCAAATG					
flsynbt.fin	.CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C..CAGC..C.					
bssyn	.CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C..CAGC..C.					
	1740*	1750*	1760*	1770*	1780*	1790*
BTHKURHD	GATCAAGTGTATTTACGTTAAGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG					
flsynbt.fin	.CAGC..C..G..C..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C					
bssyn	.CAGC..C..G..C..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C					

Fig. 1D

	1800	1810	1820	1830	1840	1850
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	ATCGAATTGAATTTGTTCCGGCAGAAGTAACCTTTGAGGCAGAATATGATTAGAAAGAG					
bssyn	.C..C..C..G..C..G..C..C..G..G.....C.....C..G..C..CC.G..G..G.					
	1860	1870	1880	1890	1900	1910
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	CACAAAAGGCGGTGAATGAGCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACAGATG					
bssyn	.T..G.....C.....C.....C..CAGCAG...C..G.....CC.G..G..C..C.					
	1920	1930	1940	1950	1960	1970
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TGACGGATTATCATATTGATCAAGTATCCAATTTAGTTGAGTGTCTATCTGATGAATTTT					
bssynC..C..C..C..C.....G..GAG...CC.G..G.....CC.GAGC..C..G..C.					
	1980	1990	2000	2010	2020	2030
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GTCTGGATGAAAAAAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTTAGTGATG					
bssyn	.C.....C..G..G..G..GC..AG.....G..G..G..C..C.....C..G..C..C.					
	2040	2050	2060	2070	2080	2090
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AGCGGAATTTACTTCAAGATCCAACTTTAGAGGGATCAATAGACAACTAGACCGTGGCT					
bssynC..CC.G..G..G..C..C.....CC.C..C.....CC.C..G..G.....C....					
	2100	2110	2120	2130	2140	2150
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GGAGAGGAAGTACGGATATTACCATCCAAGGAGGCGATGACGTATTCAAAGAGAATTACG					
bssyn	..C..C..C..C..C..C.....G..C.....C.....G.....G.....C....					
	2160	2170	2180	2190	2200	2210
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TTACGCTATTGGGTACCTTTGATGAGTGCTATCCAACGTATTTATATCAAAAAATAGATG					
bssyn	.G..C..GC....C.....C..C.....C..C..C..CC.G..C..G..G..C..C.					
	2220	2230	2240	2250	2260	2270
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AGTCGAAATTAAAAGCCTATACCCGTTACCAATTAAGAGGGTATATCGAAGATAGTCAAG					
bssyn	..AGC..GC.G..G.....C.....C.....GC.GC.C..C..C.....G..C..C..G.					
	2280	2290	2300	2310	2320	2330
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	ACTTAGAAATCTATTTAATTCGCTACAATGCCAAACACGAAACAGTAAATGTGCCAGGTA					
bssyn	..C.G..G.....CC.G..C.....C.....G.....G..C..G..C.....C..C.					
	2340	2350	2360	2370	2380	2390
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	CGGGTTCCTTATGGCCGCTTTTCAGCCCCAAGTCCAATCGGAAAATGTGCCCATCATTC					
bssyn	.C..CAG.C.G.....C..GAGC.....C..C..C.....C..G..C.....C..CAG..					

Fig. 1E

	2400	2410	2420	2430	2440	2450
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	ATCATTCTCCTTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTAT					
bssyn	.C..C...AG.C.....C..C..G..C..C..C...C.G..C.....C.G..C..G.					
	2460	2470	2480	2490	2500	2510
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GGGTGATATTCAAGATTAAGACGCAAGATGGCCATGCAAGACTAGGAAATCTAGAATTTTC					
bssynC.....C.....C..G..C.....C..CC.C..G..C..C..G..G..C.					
	2520	2530	2540	2550	2560	2570
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TCGAAGAGAAACCATTAGTAGGAGAAGCACTAGCTCGTGTGAAAAGAGCGGAGAAAAAAT					
bssyn	.G..G.....G..CC.G..G..C..G..C..G..C..C.....GC.C..C.....G..G.					
	2580	2590	2600	2610	2620	2630
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GGAGAGACAAACGTGAAAAATTGGAATGGGAAACAAATATTGTTTATAAAGAGGCAAAAG					
bssyn	..C.C.....G..C..G..GC....G.....G..C..C..C..G..C..G.....C..G.					
	2640	2650	2660	2670	2680	2690
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AATCTGTAGATGCTTTATTTGTAACTCTCAATATGATAGATTACAAGCGGATACCAACA					
bssyn	.GAGC..G..C..CC.G..C..G...AGC..G..C..CC.CC.G..G..C..C.....					
	2700	2710	2720	2730	2740	2750
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TCGCGATGATTCATGCGGCAGATAAACGCGTTCATAGCATTTCGAGAAGCTTATCTGCCTG					
bssynC.....C..C..C..C..C..G.....G..C.....C..G..C..C.....C.					
	2760	2770	2780	2790	2800	2810
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AGCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTGAAGAATTAGAAGGGCGTATTT					
bssynAGC.....C..C..C..G..C..C..C..C..C..C..G..GC.G..G..C..C..C.					
	2820	2830	2840	2850	2860	2870
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TCACTGCATTCTCCCTATATGATGCGAGAAATGTCATTAAAAATGGTGATTTTAATAATG					
bssynC..C...AG...G..C..C..CC.C..C..G..C..G..C..C..C..C..C..C.					
	2880	2890	2900	2910	2920	2930
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GCTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAAGAACAAAACAACCCGTT					
bssyn	..C.GAG.....G..C..C..G..C..G..G..G.....CA					
	2940	2950	2960	2970	2980	2990
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	CGGTCCTTGTTGTTCCGGAATGGGAAGCAGAAGTGTACACAAGAAGTTCGTGTCTGTCCGG					
bssyn	GC..G..G..G..G..C..G.....G..C..G...AGC..G..G..G..C..G..C..C.					

Fig. 1F

	3000	3010	3020	3030	3040	3050
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	GTCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGATATGGAGAAGGTTGCGTAA					
bssyn	.C..C.....C.....G..C..G..C..C.....C..C..C..G..C.....G.					

	3060	3070	3080	3090	3100	3110
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	CCATTCATGAGATCGAGAACAATACAGACGAACTGAAGTTTAGCAACTGTGTAGAAGAGG					
bssynC..C.....C.....G..C.....C.....C.....C..G..G....					

	3120	3130	3140	3150	3160	3170
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AAGTATATCCAAACAACACGGTAACGTGTAATGATTATACTGCGACTCAAGAAGAATATG					
bssyn	.G..G..C..C.....C..G..C..C..C..C..C..C..C..C..G..G..G..C.					

	3180	3190	3200	3210	3220	3230
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	AGGGTACGTACACTTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTCTTCTG					
bssynC..C.....CAGC..C..C..C..C..C.....C.....C..G.....CAGCAGC.					

	3240	3250	3260	3270	3280	3290
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	TACCAGCTGATTATGCATCAGCCTATGAAGAAAAAGCATATACAGATGGACGAAGAGACA					
bssyn	.G..C..C..C..C..C..CAGC.....C..G..G..G..C..C..C..C..C..CC.C....					

	3300	3310	3320	3330	3340	3350
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	ATCCTTGTGAATCTAACAGAGGATATGGGGATTACACACCACTACCAGCTGGCTATGTGA					
bssyn	.C..C..C..GAGC...C..C..C..C..C.....C..C..G..C..C.....C....					

	3360	3370	3380	3390	3400	3410
BTHKURHD	*	*	*	*	*	*
flsynbt.fin	CAAAAGAATTAGAGTACTTCCCAGAAACCGATAAGGTATGGATTGAGATCGGAGAAACGG					
bssyn	.C..G..GC.G.....C..G.....C.....G.....C.....C.....C..G..C.					

	3420	3430	3440	3450	3460	
BTHKURHD	*	*	*	*	*	
flsynbt.fin	AAGGAACATTCATCGTGACAGCGTGGAATTACTTCTTATGGAGGAATAA					
bssyn	.G..C..C.....GC.G..G..G.....G..G					
					...TG..G	

0998462-112001

Fig. 2A

	10	20	30	40	50	60
	*	*	*	*	*	*
BTHKURHD	ATGGATAACAATCCGAACATCAATGAATGCATTCCTTATAATTGTTTAAGTAACCCTGAA					
bssynC.....C..C.....C..G.....C..C..C..C..CC.G..C.....C..G					
	70	80	90	100	110	120
	*	*	*	*	*	*
BTHKURHD	GTAGAAGTATTAGGTGGAGAAAGAATAGAACTGGTTACACCCCAATCGATATTTTCCTTG					
bssyn	..G..G..GC.G..C..C..GC.C..C..G..C..C.....C.....C..CAG.C..					
	130	140	150	160	170	180
	*	*	*	*	*	*
BTHKURHD	TCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTGTTAGGACTA					
bssyn	AGC..G..C..G..C..GC....C..G..C..G.....C..C..C..C..C..C.G..C..G					
	190	200	210	220	230	240
	*	*	*	*	*	*
BTHKURHD	GTTGATATAATATGGGGAATTTTGGTCCCTCTCAATGGGACGCATTTCTTGTACAAATT					
bssyn	..G..C..C..C.....C..C..C..C...AGC..G.....C..C..G..G..G..C					
	250	260	270	280	290	300
	*	*	*	*	*	*
BTHKURHD	GAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA					
bssyn	..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G					
	310	320	330	340	350	360
	*	*	*	*	*	*
BTHKURHD	GAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGAT					
bssyn	..G..C..G.....C..G..C.....C.....C..GAGC..CC.C.....G..C..C					
	370	380	390	400	410	420
	*	*	*	*	*	*
BTHKURHD	CCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCC					
bssyn	..C..C..C..C..CC.GC.C..G.....C..C..G.....C.....C...					
	430	440	450	460	470	480
	*	*	*	*	*	*
BTHKURHD	CTTACAACCGCTATTCCTCTTTTGCAGTTCAAAATTATCAAGTTCCTCTTTTATCAGTA					
bssyn	..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G					
	490	500	510	520	530	540
	*	*	*	*	*	*
BTHKURHD	TATGTTCAAGCTGCAAATTTACATTTATCAGTTTGTAGAGATGTTTCAGTGTGTTGGACAA					
bssyn	..C..G..G..C..C..CC.G..CC.GAGC..GC..C..C..C..CAGC.....C..C..G					
	550	560	570	580	590	600
	*	*	*	*	*	*
BTHKURHD	AGGTGGGGATTTGATGCCGCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTATT					
bssyn	C.C.....C..C..C.....C..C.....C..C..C..C..C..CC.G..CC.C..G..C					
	610	620	630	640	650	660
	*	*	*	*	*	*
BTHKURHD	GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA					
bssynC..C..C..C..C..G.....C..C..CC.G.....C..G.....T					
	670	680	690	700	710	720
	*	*	*	*	*	*
BTHKURHD	CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAACTGTA					
bssyn	..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G					

Fig. 2B

	730	740	750	760	770	780
BTHKURHD	*	*	*	*	*	*
bssyn	TTAGATATCGTTTCTCTATTTCCGAACATGATAGTAGAACGTATCCAATTCGAACAGTT					
	C.G..C.....GAGC..G..C...C.....C..C..CC.C..C..C..C..C..C..C..G					
	790	800	810	820	830	840
BTHKURHD	*	*	*	*	*	*
bssyn	TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTTTT					
	AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C..C					
	850	860	870	880	890	900
BTHKURHD	*	*	*	*	*	*
bssyn	CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT					
	..C...AGC..C.....C..G..C..C..CC.C..C..C..CC.....C..C..G					
	910	920	930	940	950	960
BTHKURHD	*	*	*	*	*	*
bssyn	AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA					
C..C.....C..C..C..C..CC.C..C..G..C..C..AGC..C..C..G					
	970	980	990	1000	1010	1020
BTHKURHD	*	*	*	*	*	*
bssyn	ATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACTTTTCCGCTATATGGAAC					
	..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C					
	1030	1040	1050	1060	1070	1080
BTHKURHD	*	*	*	*	*	*
bssyn	ATGGGAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGA					
C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C					
	1090	1100	1110	1120	1130	1140
BTHKURHD	*	*	*	*	*	*
bssyn	ACATTATCGTCCACTTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAAC					
	..CC.GAGCAG...CC.G..CC.TC.....C..C..C..C..C..C..C..G..G..G					
	1150	1160	1170	1180	1190	1200
BTHKURHD	*	*	*	*	*	*
bssyn	TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA					
	AGC..G..G.....C..C..G..C..C..C..C..C..AG.AGC..CC....CAG...C..G					
	1210	1220	1230	1240	1250	1260
BTHKURHD	*	*	*	*	*	*
bssyn	TACAGAAAAGCGGAACGGTAGATTGCTGGATGAAATACCGCCACAGAATAACAACGTG					
	...C..C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.....					
	1270	1280	1290	1300	1310	1320
BTHKURHD	*	*	*	*	*	*
bssyn	CCACCTAGGCAAGGATTTAGTCATCGATTAAAGCCATGTTTCAATGTTTCGTTTCAGGCTTT					
C.A..G..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C					
	1330	1340	1350	1360	1370	1380
BTHKURHD	*	*	*	*	*	*
bssyn	AGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCT					
	..C..C..C..C..G..C..C..CC.T..A.....AGC.....T..C..C.....C					
	1390	1400	1410	1420	1430	
BTHKURHD	*	*	*	*	*	
bssyn	GAATTTAATAATATAATTCCTTCATCA--CAAATTACACAAATACCTTTAACAAAATCTA					
	..G..C..C..C..C..C..C..G..GC..G..C..C..G..C..CC.G..C..GAGC.					

0998462-112001

Fig. 3A

	10	20	30	40	50	60
syn1T.mze	ATGGACAACAACCCCAACATCAACGAGTGCATCCCCTACAACCTGCCTGAGCAACCCCGAG					
bssyn					
synful.mod					
	70	80	90	100	110	120
syn1T.mze	GTGGAGGTGCTGGGCGGCGAGCGCATCGAGACCGGCTACACCCCATCGACATCAGCCTG					
bssyn					
synful.mod					
	130	140	150	160	170	180
syn1T.mze	AGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCCGGCGCCGGCTTCGTGCTGGGCCTG					
bssyn					
synful.mod					
	190	200	210	220	230	240
syn1T.mze	GTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGACGCCTTCCTGGTGCAGATC					
bssyn					
synful.mod					
	250	260	270	280	290	300
syn1T.mze	GAGCAGCTGATCAACCAGCGCATCGAGGAGTTCGCCCCGAACCAGGCCATCAGCCGCCTG					
bssyn					
synful.mod					
	310	320	330	340	350	360
syn1T.mze	GAGGGCCTGAGCAACCTGTACCAGATCTACGCCGAGAGCTTCCGCGAGTGGGAGGCCGAC					
bssynA.....					
synful.modA.....					
	370	380	390	400	410	420
syn1T.mze	CCCACCAACCCCGCCCTGCGCGAGGAGATGCGCATCCAGTTCAACGACATGAACAGCGCC					
bssyn					
synful.mod					
	430	440	450	460	470	480
syn1T.mze	CTGACCACCGCCATCCCCCTGTTTCGCCGTGCAGAACTACCAGGTGCCCTGCTGAGCGTG					
bssyn					
synful.mod					
	490	500	510	520	530	540
syn1T.mze	TACGTGCAGGCCGCCAACCTGCACCTGAGCGTGCTGCGCGACGTGAGCGTGTTCGGCCAG					
bssynC.....					
synful.modC.....					
	550	560	570	580	590	600
syn1T.mze	CGCTGGGGCTTCGACGCCGCCACCATCAACAGCCGCTACAACGACCTGACCCGCCTGATC					
bssyn					
synful.mod					

09988462-112001

Fig. 3B

	610	620	630	640	650	660
syn1T.mze	*	*	*	*	*	*
bssyn	GGCAACTACACCGACCACGCCGTGCGCTGGTACAACACCGGCCTGGAGCGCGTGTGGGGC					T
synful.mod	T
	670	680	690	700	710	720
syn1T.mze	*	*	*	*	*	*
bssyn	CCCGACAGCCGCGACTGGATCCGCTACAACCCAGTTCCGCCGCGAGCTGACCCTGACCGTG		A.G			
synful.mod	A.G
	730	740	750	760	770	780
syn1T.mze	*	*	*	*	*	*
bssyn	CTGGACATCGTGAGCCTGTTCCCCAACTACGACAGCCGCACCTACCCCATCCGCACCGTG					
synful.mod
	790	800	810	820	830	840
syn1T.mze	*	*	*	*	*	*
bssyn	AGCCAGCTGACCCGCGAGATCTACACCAACCCCGTGCTGGAGAACTTCGACGGCAGCTTC		T			
synful.mod	T
	850	860	870	880	890	900
syn1T.mze	*	*	*	*	*	*
bssyn	CGCGGCAGCGCCCAGGGCATCGAGGGCAGCATCCGCAGCCCCACCTGATGGACATCCTG					
synful.mod
	910	920	930	940	950	960
syn1T.mze	*	*	*	*	*	*
bssyn	AACAGCATCACCATCTACACCGACGCCCACCGCGGCGAGTACTACTGGAGCGGCCACCAG					
synful.mod
	970	980	990	1000	1010	1020
syn1T.mze	*	*	*	*	*	*
bssyn	ATCATGGCCAGCCCCGTGGGCTTCAGCGGCCCGAGTTACCTTCCCCCTGTACGGCACC		C			
synful.mod	C
	1030	1040	1050	1060	1070	1080
syn1T.mze	*	*	*	*	*	*
bssyn	ATGGGCAACGCGCCCCCAGCAGCGCATCGTGGCCAGCTGGGCCAGGGCGTGTACCGC		T	A	T	
synful.mod	T	A	T	A
	1090	1100	1110	1120	1130	1140
syn1T.mze	*	*	*	*	*	*
bssyn	ACCCTGAGCAGCACCTGTACCGCGCCCTTCAACATCGGCATCAACAACCAGCAGCTG		T	A	T	
synful.mod	T	A	T
	1150	1160	1170	1180	1190	1200
syn1T.mze	*	*	*	*	*	*
bssyn	AGCGTGCTGGACGGCACCGAGTTCGCCTACGGCACCAGCAGCAACCTGCCAGCGCCGTG					
synful.mod

09988462 112001

Fig. 3C

	1210*	1220*	1230*	1240*	1250*	1260*
syn1T.mze	TACCGCAAGAGCGGCACCGTGGACAGCCTGGACGAGATCCCCCCCCAGAACAACAACGTG					
bssynT.....					
synful.modT.....					
	1270*	1280*	1290*	1300*	1310*	1320*
syn1T.mze	CCCCCGCCAGGGCTTCAGCCACCGCCTGAGCCACGTGAGCATGTTCCGCGAGCGGCTTC					
bssyn	..A..T..A.....T.....T.....					
synful.mod	..A..T..A.....T.....T.....					
	1330*	1340*	1350*	1360*	1370*	1380*
syn1T.mze	AGCAACAGCAGCGTGAGCATCATCCGCGCCCCATGTTTCAGCTGGATCCACCGCAGCGCC					
bssynT..A..T.....T.....T...					
synful.modT..A..T.....T.....T...					
	1390*	1400*	1410*	1420*	1430*	1440*
syn1T.mze	GAGTTCAACAACATCATCCCCAGCAGCCAGATCACCAGATCCCCCTGACCAAGAGCACC					
bssyn					
synful.mod					
	1450*	1460*	1470*	1480*	1490*	1500*
syn1T.mze	AACCTGGGCAGCGGCACCAGCGTGGTGAAGGGCCCCGGCTTCACCGGCGGCGACATCCTG					
bssyn					
synful.mod					
	1510*	1520*	1530*	1540*	1550*	1560*
syn1T.mze	CGCCGCACCAGCCCCGGCCAGATCAGCACCCTGCGCGTGAACATCACCGCCCCCCTGAGC					
bssyn					
synful.mod					
	1570*	1580*	1590*	1600*	1610*	1620*
syn1T.mze	CAGCGCTACCGCGTGCGCATCCGCTACGCCAGCACCACCAACCTGCAGTTCCACACCAGC					
bssynC.....					
synful.modC.....					
	1630*	1640*	1650*	1660*	1670*	1680*
syn1T.mze	ATCGACGGCCGCCCATCAACCAGGGCAACTTCAGCGCCACCATGAGCAGCGGCAGCAAC					
bssyn					
synful.mod					
	1690*	1700*	1710*	1720*	1730*	1740*
syn1T.mze	CTGCAGAGCGGCAGCTTCCGCACCGTGGGCTTCACCACCCCCTTCAACTTCAGCAACGGC					
bssyn					
synful.mod					
	1750*	1760*	1770*	1780*	1790*	1800*
syn1T.mze	AGCAGCGTGTTTACCCTGAGCGCCACGTGTTCAACAGCGGCAACGAGGTGTACATCGAC					
bssyn					
synful.mod					

Fig. 3D

	1810	1820	1830	1840	1850	1860
syn1T.mze	*	*	*	*	*	*
bssyn	CGCATCGAGTTCGTGCCCCGCCGAGGTGACCTTCGAGGCCGAGTACGACCTGGAGCGCGCC					A.G..T
synful.mod	A.G..T
	1870	1880	1890	1900	1910	1920
syn1T.mze	*	*	*	*	*	*
bssyn	CAGAAGGCCGTGAACGAGCTGTTACCAGCAGCAACCAGATCGGCCTGAAGACCGACGTG					
synful.mod
	1930	1940	1950	1960	1970	1980
syn1T.mze	*	*	*	*	*	*
bssyn	ACCGACTACCACATCGACCAGGTGAGCAACCTGGTGGAGTGCCTGAGCGACGAGTTCTGC					
synful.mod	T.....	-----	-----	-----	-----
	1990	2000	2010	2020	2030	2040
syn1T.mze	*	*	*	*	*	*
bssyn	CTGGACGAGAAGAAGGAGCTGAGCGAGAAGGTGAAGCACGCCAAGCGCCTGAGCGACGAG					
synful.mod	-----	-----	-----	-----	-----	-----
	2050	2060	2070	2080	2090	2100
syn1T.mze	*	*	*	*	*	*
bssyn	CGCAACCTGCTGCAGGACCCCAACTTCCGCGGCATCAACCGCCAGCTGGACCGCGGCTGG					
synful.mod	-----	-----	-----	-----	-----	-----
	2110	2120	2130	2140	2150	2160
syn1T.mze	*	*	*	*	*	*
bssyn	CGCGGCAGCACCGACATCACCATCCAGGGCGGCGACGACGTGTTCAAGGAGAACTACGTG					
synful.mod	-----	-----	-----	-----	-----	-----
	2170	2180	2190	2200	2210	2220
syn1T.mze	*	*	*	*	*	*
bssyn	ACCCTGCTGGGCACCTTCGACGAGTGCTACCCACCTACCTGTACCAGAAGATCGACGAG					
synful.mod	-----	-----	-----	-----	-----	-----
	2230	2240	2250	2260	2270	2280
syn1T.mze	*	*	*	*	*	*
bssyn	AGCAAGCTGAAGGCCTACACCCGCTACCAGCTGCGCGGCTACATCGAGGACAGCCAGGAC					
synful.mod	-----	-----	-----	-----	-----	-----
	2290	2300	2310	2320	2330	2340
syn1T.mze	*	*	*	*	*	*
bssyn	CTGGAGATCTACCTGATCCGCTACAACGCCAAGCACGAGACCGTGAACGTGCCCCGGCACC					
synful.mod	-----	-----	-----	-----	-----	-----
	2350	2360	2370	2380	2390	2400
syn1T.mze	*	*	*	*	*	*
bssyn	GGCAGCCTGTGGCCCCCTGAGCGCCCCCAGCCCCATCGGCAAGTGCGCCACACAGCCAC					
synful.mod	-----	-----	-----	-----	-----	-----

Fig. 3E

	2410*	2420*	2430*	2440*	2450*	2460*
syn1T.mze	CACTTCAGCCTGGACATCGACGTGGGCTGCACCGACCTGAACGAGGACCTGGGCGTGTGG					
bssyn	-----					
synful.mod					
	2470*	2480*	2490*	2500*	2510*	2520*
syn1T.mze	GTGATCTTCAAGATCAAGACCCAGGACGGCCACGCCCCTGGGCAACCTGGAGTTCCTG					
bssyn	-----					
synful.mod					
	2530*	2540*	2550*	2560*	2570*	2580*
syn1T.mze	GAGGAGAAGCCCCTGGTGGGCGAGGCCCTGGCCCCGCTGAAGCGCGCCGAGAAGAAGTGG					
bssyn	-----					
synful.mod					
	2590*	2600*	2610*	2620*	2630*	2640*
syn1T.mze	CGCGACAAGCGCGAGAAGCTGGAGTGGGAGACCAACATCGTGTACAAGGAGGCCAAGGAG					
bssyn	-----					
synful.mod					
	2650*	2660*	2670*	2680*	2690*	2700*
syn1T.mze	AGCGTGGACGCCCTGTTCGTGAACAGCCAGTACGACCGCTGCAGGCCGACACCAACATC					
bssyn	-----					
synful.mod					
	2710*	2720*	2730*	2740*	2750*	2760*
syn1T.mze	GCCATGATCCACGCCGCCGACAAGCGCGTGCACAGCATCCGCGAGGCCTACCTGCCCCGAG					
bssyn	-----					
synful.modT.....					
	2770*	2780*	2790*	2800*	2810*	2820*
syn1T.mze	CTGAGCGTGATCCCCGGCGTGAACGCCGCCATCTTCGAGGAGCTGGAGGGCCGCATCTTC					
bssyn	-----					
synful.mod					
	2830*	2840*	2850*	2860*	2870*	2880*
syn1T.mze	ACCGCCTTCAGCCTGTACGACGCCCGCAACGTGATCAAGAACGGCGACTTCAACAACGGC					
bssyn	-----					
synful.mod					
	2890*	2900*	2910*	2920*	2930*	2940*
syn1T.mze	CTGAGCTGCTGGAACGTGAAGGGCCACGTGGACGTGGAGGAGCAGAACAACCACCGCAGC					
bssyn	-----					
synful.mod					
	2950*	2960*	2970*	2980*	2990*	3000*
syn1T.mze	GTGCTGGTGGTGCCCGAGTGGGAGGCCGAGGTGAGCCAGGAGGTGCGCGTGTGCCCCGGC					
bssyn	-----					
synful.mod					

0908462-11001

Fig. 3F

	3010	3020	3030	3040	3050	3060
	*	*	*	*	*	*
syn1T.mze	CGCGGCTACATCCTGCGCGTGACCGCCTACAAGGAGGGCTACGGCGAGGGCTGCGTGACC					
bssyn	-----					
synful.mod					
	3070	3080	3090	3100	3110	3120
	*	*	*	*	*	*
syn1T.mze	ATCCACGAGATCGAGAACAACACCGACGAGCTGAAGTTCAGCAACTGCGTGAGGAGGAG					
bssyn	-----					
synful.modC.....					
	3130	3140	3150	3160	3170	3180
	*	*	*	*	*	*
syn1T.mze	GTGTACCCCAACAACACCGTGACCTGCAACGACTACACCGCCACCCAGGAGGAGTACGAG					
bssyn	-----					
synful.mod					
	3190	3200	3210	3220	3230	3240
	*	*	*	*	*	*
syn1T.mze	GGCACCTACACCAGCCGCAACCGCGGCTACGACGGCGCCTACGAGAGCAACAGCAGCGTG					
bssyn	-----					
synful.mod					
	3250	3260	3270	3280	3290	3300
	*	*	*	*	*	*
syn1T.mze	CCCGCCGACTACGCCAGCGCCTACGAGGAGAAGGCCTACACCGACGGCCGCCGCGACAAC					
bssyn	-----					
synful.mod					
	3310	3320	3330	3340	3350	3360
	*	*	*	*	*	*
syn1T.mze	CCCTGCGAGAGCAACCGCGGCTACGGCGACTACACCCCCTGCCCGCCGGCTACGTGACC					
bssyn	-----					
synful.mod					
	3370	3380	3390	3400	3410	3420
	*	*	*	*	*	*
syn1T.mze	AAGGAGCTGGAGTACTTCCCCGAGACCGACAAGGTGTGGATCGAGATCGGCGAGACCGAG					
bssyn	-----					
synful.mod					
	3430	3440	3450	3460		
	*	*	*	*		
syn1T.mze	GGCACCTTCATCGTGGACAGCGTGGAGCTGCTGCTGATGGAGGAGTAG					
bssyn	-----					
synful.mod					

09988462-112001

Fig. 4A

	10	20	30	40	50	60
BTHKURHD	ATGGATAACAATCCGAACATCAATGAATGCATTCCCTTATAATTGTTTAAGTAACCCCTGAA					
PMONBTC.....C..A.....C.....A..C..C..C..G.....A...					
bssynC.....C..C.....C..G.....C..C..C..CC.G..C.....C..G					
	70	80	90	100	110	120
BTHKURHD	GTAGAAGTATTAGGTGGAGAAAGAATAGAACTGGTTACACCCCAATCGATATTTTCCTTG					
PMONBT	..T.....C..T.....C..C..T.....C.....T..C.....C..C.....					
bssyn	..G..G..GC.G..C..C..GC.C..C..G..C..C.....C.....C..CAG.C..					
	130	140	150	160	170	180
BTHKURHD	TCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTGTTAGGACTA					
PMONBT	..CT.G..A..G.....GC.C..C..G..C..G..A.....G..C..TC.C.....					
bssyn	AGC..G..C..G..C..GC....C..G..C..G.....C..C..C..C..C..G..C..G					
	190	200	210	220	230	240
BTHKURHD	GTTGATATAATATGGGGAATTTTGGTCCCTCTCAATGGGACGCATTTCTTGACAAATT					
PMONBTC..C..C.....T..C.....A.....T.....C..G..G.....					
bssyn	..G..C..C..C.....C..C..C..C...AGC..G.....C..C..G..G..G..C					
	250	260	270	280	290	300
BTHKURHD	GAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA					
PMONBT	..G.....G..C.....G..G..C.....G.....C.....G.....C.....G..G					
bssyn	..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G					
	310	320	330	340	350	360
BTHKURHD	GAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGAT					
PMONBTT.G.....C..C.....C..T.....GAGC..C.....C.....C..C					
bssyn	..G..C..G.....C..G..C.....C.....C..GAGC..CC.C.....G..C..C					
	370	380	390	400	410	420
BTHKURHD	CCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCC					
PMONBTC.....TC.CC.C..G..A.....C.....C.....C.....C...					
bssyn	..C..C..C..C..CC.GC.C..G.....C..C..G.....C.....C.....C...					
	430	440	450	460	470	480
BTHKURHD	CTTACAACCGCTATTCCCTCTTTTGCAGTTCAAATTATCAAGTTCCTCTTTTATCAGTA					
PMONBT	T.G..C..A.....C..AT.G..C.....C..G..C..C.....C..G..C..G					
bssyn	..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G					
	490	500	510	520	530	540
BTHKURHD	TATGTTCAAGCTGCAAATTTACATTTATCAGTTTGGAGAGATGTTTCAGTGTGGACAA					
PMONBT	..C.....A..T..C..T..CC.CAGC..GC.TC....C..AGC.....G..G					
bssyn	..C..G..G..C..C..CC.G..CC.GAGC..GC..C..C..C..CAGC.....C..C..G					
	550	560	570	580	590	600
BTHKURHD	AGGTGGGGATTTGATGCCGCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTATT					
PMONBTC.....T..A..C.....C.....C..C..C..C..CC.T.....G..C					
bssyn	C.C.....C..C..C.....C..C.....C..C..C..C..C..CC.G..CC.C..G..C					

09988462.112001

Fig. 4B

	610	620	630	640	650	660
BTHKURHD	*	*	*	*	*	*
PMONBT	GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA					
bssyn	..A.....C..C..C..C.....T..T.....C..T..C..G.....C.....T					
	670	680	690	700	710	720
BTHKURHD	*	*	*	*	*	*
PMONBT	CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAAGTGA					
bssyn	..T.....CAGCC..C..C.....T.....C..C..G..C..G.....G..C..C..A..T					
	730	740	750	760	770	780
BTHKURHD	*	*	*	*	*	*
PMONBT	TTAGATATCGTTTCTCTATTTCCGAACATGATAGTAGAACGTATCCAATTCGAACAGTT					
bssyn	..G..C..T..G.....C..C.....CTCC.....C..C..T..C..T.....G					
	790	800	810	820	830	840
BTHKURHD	*	*	*	*	*	*
PMONBT	TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAAATTTGATGGTAGTTTT					
bssyn	..C..T..C.....C.....T.....TC..T..G..C..C..C.....C..C					
	850	860	870	880	890	900
BTHKURHD	*	*	*	*	*	*
PMONBT	CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT					
bssyn	..T..T..T..C..A..T..C.....CTCC..C.....C.....C..CT..G					
	910	920	930	940	950	960
BTHKURHD	*	*	*	*	*	*
PMONBT	AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA					
bssynC.....T.....C..GC.....C.....C.....G.....C.....T..A..C..G					
	970	980	990	1000	1010	1020
BTHKURHD	*	*	*	*	*	*
PMONBT	ATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACCTTTTCCGCTATATGGAAC					
bssyn	..C.....C.....A..T..A..CAGC.....C..G..T..C.....T..C.....C.....C					
	1030	1040	1050	1060	1070	1080
BTHKURHD	*	*	*	*	*	*
PMONBT	ATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCACTAGGTCAGGGCGTGTATAGA					
bssynC..C.....T..A..T..G..G..C..C..G..A..G..G..C.....T..C..C..C					
	1090	1100	1110	1120	1130	1140
BTHKURHD	*	*	*	*	*	*
PMONBT	ACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAACAACACTA					
bssyn	..C..G..T.....C..G..C.....C..C.....C..T..C..C..C..G.....T					
	1150	1160	1170	1180	1190	1200
BTHKURHD	*	*	*	*	*	*
PMONBT	TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA					
bssyn	..C.....A.....G..C..C.....T..T..C.....C.....C.....C.....T					

09588462-112001

Fig. 4C

	1210*	1220*	1230*	1240*	1250*	1260*
BTHKURHD	TACAGAAAAAGCGGAACGGTAGATTCGCTGGATGAAATACCGCCACAGAATAACAACGTG					
PMONBT	...G...C...T...CT...C...C...A...C...T...					
bssyn	...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.....					
	1270*	1280*	1290*	1300*	1310*	1320*
BTHKURHD	CCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTTTCAGGCTTT					
PMONBTC.....CTCC..CA.G..G.....C..G..C.....C.....C..A..C					
bssynC.A..G..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C					
	1330*	1340*	1350*	1360*	1370*	1380*
BTHKURHD	AGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGATACATCGTAGTGCT					
PMONBT	..C..C...TCC..G..C..C..C.....A.....T.....C..C.....C					
bssyn	..C..C..C..C..G..C..C..CC.T..A.....AGC.....T..C..C.....C					
	1390*	1400*	1410*	1420*	1430*	
BTHKURHD	GAATTTAATAATATAATTCCTTCATCA					CAAATTACACAAATACCTTTAACAAAATCTA
PMONBT	..G..C..C.....C.....C..T.....C..C.....C..A..G..C..G..GAGC..					
bssyn	..G..C..C..C..C..C.....G..GC..G..C..C..G..C..CC.G..C..GAGC..					
	1440*	1450*	1460*	1470*	1480*	1490*
BTHKURHD	CTAATCTTGGCTCTGGAACCTTCTGTCGTTAAAGGACCAGGATTTACAGGAGGAGATATTC					
PMONBT	..C.....A.....G.....C..C.....C..C.....C..T.....C..C..C..					
bssyn	..C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C..					
	1500*	1510*	1520*	1530*	1540*	1550*
BTHKURHD	TTCGAAGAACTTCACCTGGCCAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT					
PMONBT	..A.....T.....AGC...C.C...T..C..C.....C.T.....C.T.					
bssyn	.G..CC.C..CAGC..C.....CAGC...C.GC.C..G..C..C..C..C..CC.GA					
	1560*	1570*	1580*	1590*	1600*	1610*
BTHKURHD	CACAAAGATATCGGGTAAGAATTGCTACGCTTCTACCACAAATTTACAATTCATACAT					
PMONBT	.T.....T..C..G.....T.....A.....T..C..G.....C..C..					
bssyn	GC..GC.C..C..C..CC.C..C.....CAGC.....C..CC.G..G.....C..CA					
	1620*	1630*	1640*	1650*	1660*	1670*
BTHKURHD	CAATTGACGGAAGACCTATTAATCAGGGGAATTTTTCAGCAACTATGAGTAGTGGGAGTA					
PMONBT	.C..C.....G.....C.....T..C..C..C.....C..TCA..C..C..C..					
bssyn	GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C..					
	1680*	1690*	1700*	1710*	1720*	1730*
BTHKURHD	ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTACTACTCCGTTTAACTTTTCAAATG					
PMONBT	.C..G..A.....C.....C..A..C..C.....C.....T..C.....C..T..C..					
bssyn	..CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C..CAGC..C..					
	1740*	1750*	1760*	1770*	1780*	1790*
BTHKURHD	GATCAAGTGTATTTACGTTAAGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG					
PMONBTC..T..C..CC.T..C.....G.....T.....C.....G..C..T..					
bssyn	.CAGC..C..G..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C..					

Fig. 4D

	1800	1810	1820	1830	1840
	*	*	*	*	*
BTHKURHD	ATCGAATTGAATTTGTTCCGGCAGAAGTAACCTTTGAGGCAGAATA-----				
PMONBT	.C..T.....G.....G..T..C.....T.....C.....T..G..-----				
bssyn	.C..C..C..G..C..G..C..C..G..G.....C.....C..G..CGACCTGGAGAGGG				

BTHKURHD	CTCAGAAGGCCGTGAACGAGCTGTTACACGAGCAGCAACCAGATCGGCCTGAAGACCGACG				
PMONBT	-----				
bssyn	TGACCGACTACCACATCGATCAGGTGTAG				

09988462 112001

Fig. 5A

	10	20	30	40	50	60
PMONBT	ATGGACAACAACCCAAACATCAACGAATGCATTCCATACAAGTCTTGAGTAACCCAGAA					
bssynC.....G.....C..C.....C.....C.....C..G					
	70	80	90	100	110	120
PMONBT	GTTGAAGTACTTGGTGGAGAACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG					
bssyn	..G..G..G..G..C..C..G.....C..G.....C.....C.....AG.C..					
	130	140	150	160	170	180
PMONBT	TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTGCTGGGTTCTCTCGGACTA					
bssyn	AG.C.....C.....C.....G.....C..C..C..C.....G..G..C..G					
	190	200	210	220	230	240
PMONBT	GTTGACATCATCTGGGGTATCTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT					
bssyn	..G.....C.....C..C..CAGC..G.....C..C.....G..C					
	250	260	270	280	290	300
PMONBT	GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGAACCAGGCCATCTCTAGGTTG					
bssynC.....C..C.....G.....C..C.....AGCC.CC..					
	310	320	330	340	350	360
PMONBT	GAAGGATTGAGCAATCTCTACCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT					
bssyn	..G..CC.....C..G.....C..C.....C..C.....G.....C					
	370	380	390	400	410	420
PMONBT	CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAATTCAACGACATGAACAGCGCC					
bssyn	..C..C.....C..C..G.....G.....C..C..G.....					
	430	440	450	460	470	480
PMONBT	TTGACCACAGCTATCCCATTGTTTCGAGTCCAGAACTACCAAGTTCCTCTCTGTCCGTG					
bssyn	C.....C..C.....CC.....C..G.....G.....G..G..C..GC..AG....					
	490	500	510	520	530	540
PMONBT	TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAGACGTTAGCGTGTTTGGGCAA					
bssynG..G..C..C..C..G.....G.....G..C.....C.....C..C..G					
	550	560	570	580	590	600
PMONBT	AGGTGGGGATTTCGATGCTGCAACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT					
bssyn	C.C.....C.....C..C..C.....C.....C.....G..CC.C.....C					
	610	620	630	640	650	660
PMONBT	GGAAACTACACCGACCACGCTGTTTCGTTGGTACAACACTGGCTTGGAGCGTGTCTGGGGT					
bssyn	..C.....C.....C..G..C.....C.....C..C.....C..G.....					
	670	680	690	700	710	720
PMONBT	CCTGATTCTAGAGATTGGATTAGATACAACAGTTCAGGAGAGAATTGACCCCTCAGATT					
bssyn	..C..CAGCC.C..C.....C..G.....C..CC.C..GC.....G..C..G					

09988462.112001

Fig. 5B

	730	740	750	760	770	780
PMONBT	TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAACCTACCCTATCCGTACAGTG					
bssyn	C.....C...AGC..G.....C.....C...AG.C.C.....C.....C..C...					
	790	800	810	820	830	840
PMONBT	TCCCAACTTACCAGAGAAATCTATACTAACCAGTTCTTGAGAACTTCGACGGTAGCTTC					
bssyn	AG...G..G...C.C..G..T..C..C.....C..G..G.....C.....					
	850	860	870	880	890	900
PMONBT	CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCCACACTTGATGGACATCTTG					
bssyn	..C..CAGC.....G..C.....G...AG....C.C.....C...C.....C..					
	910	920	930	940	950	960
PMONBT	AACAGCATAACTATCTACAGCGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG					
bssynC..C.....C...C..C...C.C..C.....C.....AGC..C.....					
	970	980	990	1000	1010	1020
PMONBT	ATCATGGCCTCTCCAGTTGGATTTCAGCGGGCCGAGTTTACCTTTCTCTCTATGGAAGT					
bssynAGC..C..C..C.....C.....C.....C...C..G..C..C..C..C					
	1030	1040	1050	1060	1070	1080
PMONBT	ATGGGAAACGCCGCTCCACAACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA					
bssynC.....T..A..T..G..G..C.....G..A..G..G..C.....A..G...C.C					
	1090	1100	1110	1120	1130	1140
PMONBT	ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCGGTATCAACAACCAGCAACTT					
bssyn	...C..AGCAG....C.....C.TC....T.....C.....C.....G..G					
	1150	1160	1170	1180	1190	1200
PMONBT	TCCGTTCTTGACGGAACAGAGTTTCGCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT					
bssyn	AG...G..G.....C..C.....C..C...AGCAGC...C....CAG...C..G					
	1210	1220	1230	1240	1250	1260
PMONBT	TACAGAAAGAGCGGAACCGTTGATTCTTGGACGAAATCCCACCACAGAACAACAATGTG					
bssyn	...C.C.....C.....G..CAG.C.....G.....C..T.....C...					
	1270	1280	1290	1300	1310	1320
PMONBT	CCACCCAGGCAAGGATTCTCCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTTC					
bssynTC.A..G..C...AG....C.TC.....AG.....CAGT..C...					
	1330	1340	1350	1360	1370	1380
PMONBT	AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCTCATGGATTTCATCGTAGTGCT					
bssynCAG.....C.T..A.....AGC.....C..C.....C					
	1390	1400	1410	1420	1430	1440
PMONBT	GAGTTCAACAATATCATTCCTTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT					
bssynC.....C..CAG.AGC..G.....G.....CC.....AGC..C					

09988462-12001

Fig. 5C

	1450	1460	1470	1480	1490	1500
PMONBT	*	*	*	*	*	*
bssyn	AACCTTGGATCTGGAACCTTCTGTCGTGAAAGGACCAGGCTTCACAGGAGGTGATATTCTT					
G..CAGC..C..CAGC..G.....G..C..C.....C..C..C..C..G					
	1510	1520	1530	1540	1550	1560
PMONBT	*	*	*	*	*	*
bssyn	AGAAGAACTTCTCCTGGCCAGATTAGCACCTCAGAGTTAACATCACTGCACCACTTTCT					
	C.CC.C..CAGC..C.....C.....GC.C..G.....C..C..C..GAGC					
	1570	1580	1590	1600	1610	1620
PMONBT	*	*	*	*	*	*
bssyn	CAAAGATATCGTGTGTCAGGATTCGTTACGCATCTACCACTAACTTGCAATTCCACACCTCC					
	..GC.C..C..C..C..C..C..C.....CAGC.....C..C....G.....AG.					
	1630	1640	1650	1660	1670	1680
PMONBT	*	*	*	*	*	*
bssyn	ATCGACGGAAGGCCTATCAATCAGGGTAACTTCTCCGCAACCATGTCAAGCGGCAGCAAC					
CC.C..C.....C.....C.....AG...C.....AGC.....					
	1690	1700	1710	1720	1730	1740
PMONBT	*	*	*	*	*	*
bssyn	TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTCCTTTCACTTCTCTAACGGA					
	C....GAG.....C.C.....G..C.....C..C..C.....AGC.....C					
	1750	1760	1770	1780	1790	1800
PMONBT	*	*	*	*	*	*
bssyn	TCAAGCGTTTTTACCCTTAGCGCTCATGTGTTCAATTCTGGCAATGAAGTGTACATTGAC					
	AGC.....G.....G.....C..C.....CAGC.....C..G.....C...					
	1810	1820	1830	1840		
PMONBT	*	*	*	*		
bssyn	CGTATTGAGTTTGTGCCTGCCGAAGTTACCTTCGAGGCTGAGTA-----					
	..C..C.....C.....C.....G..G.....C.....CGACCTGGAGAGGGCT					
PMONBT	-----					
bssyn	CAGAAGGCCGTGAACGAGCTGTTACCAGCAGCAACCAGATCGGCCTGAAGACCGACGTG					
PMONBT	-----C					
bssyn	ACCGACTACCACATCGATCAGGTGTAG					

0998462-11001

Fig. 6A

64 ATGGACCTGC TGCCCGACGC CCGCATCGAG GACAGCCTGT GCATCGCCGA GGGCAACAAC
MetAspLeu LeuProAsp AlaArgIleGlu AspSerLeu CysIleAla GluGlyAsnAsn

124 ATCGACCCCT TCGTGAGCGC CAGCACCGTG CAGACCGGCA TCAACATCGC CGGCCGCATC
IleAspPro PheValSer AlaSerThrVal GlnThrGly IleAsnIle AlaGlyArgIle

184 CTGGGCGTGC TGGGCGTGCC CTTGCGCGGC CAGCTGGCCA GCTTCTACAG CTTCTGGTG
LeuGlyVal LeuGlyVal ProPheAlaGly GlnLeuAla SerPheTyr SerPheLeuVal

244 GGCGAGCTGT GGCCCCGCGG CCGCGACCAG TGGGAGATCT TCCTGGAGCA CGTGGAGCAG
GlyGluLeu TrpProArg GlyArgAspGln TrpGluIle PheLeuGlu HisValGluGln

304 CTGATCAACC AGCAGATCAC CGAGAACGCC CGCAACACCG CCCTGGCCCG CCTGCAGGGC
LeuIleAsn GlnGlnIle ThrGluAsnAla ArgAsnThr AlaLeuAla ArgLeuGlnGly

364 CTGGGCGACA GCTTCCGCGC CTACCAGCAG AGCCTGGAGG ACTGGCTGGA GAACCGCGAC
LeuGlyAsp SerPheArg AlaTyrGlnGln SerLeuGlu AspTrpLeu GluAsnArgAsp

424 GACGCCCCGA CCCGCGAGCGT GCTGTACACC CAGTACATCG CCCTGGAGCT GGACTTCCTG
AspAlaArg ThrArgSer ValLeuTyrThr GlnTyrIle AlaLeuGlu LeuAspPheLeu

484 AACGCCATGC CCCTGTTTCGC CATCCGCAAC CAGGAGGTGC CCCTGCTGAT GGTGTACGCC
AsnAlaMet ProLeuPhe AlaIleArgAsn GlnGluVal ProLeuLeu MetValTyrAla

544 CAGGCCGCCA ACCTGCACCT GCTGCTGCTG CGCGACGCCA GCCTGTTCCG CAGCGAGTTC
GlnAlaAla AsnLeuHis LeuLeuLeuLeu ArgAspAla SerLeuPhe GlySerGluPhe

604 GGCCTGACCA GCCAGGAGAT CCAGCGCTAC TACGAGCGCC AGGTGGAGCG CACCCGCGAC
GlyLeuThr SerGlnGlu IleGlnArgTyr TyrGluArg GlnValGlu ArgThrArgAsp

664 TACAGCGACT ACTGCGTGGA GTGGTACAAC ACCGGCCTGA ACAGCCTGCG CGGCACCAAC
TyrSerAsp TyrCysVal GluTrpTyrAsn ThrGlyLeu AsnSerLeu ArgGlyThrAsn

724 GCCGCCAGCT GGGTGCCTA CAACCAGTTC CGCCGCGACC TGACCCTGGG CGTGCTGGAC
AlaAlaSer TrpValArg TyrAsnGlnPhe ArgArgAsp LeuThrLeu GlyValLeuAsp

784 CTGGTGGCCC TGTTCCCCAG CTACGACACC CGCACCTACC CCATCAACAC CAGCGCCCAG
LeuValAla LeuPhePro SerTyrAspThr ArgThrTyr ProIleAsn ThrSerAlaGln

844 CTGACCCGCG AGGTGTACAC CGACGCCATC GGCGCCACCG GCGTGAACAT GGCCAGCATG
LeuThrArg GluValTyr ThrAspAlaIle GlyAlaThr GlyValAsn MetAlaSerMet

904 AACTGGTACA ACAACAACGC CCCCAGCTTC AGCGCCATCG AGGCCGCCGC CATCCGCAGC
AsnTrpTyr AsnAsnAsn AlaProSerPhe SerAlaIle GluAlaAla AlaIleArgSer

964 CCCCACCTGC TGGACTTCCT GGAGCAGCTG ACCATCTTCA GCGCCAGCAG CCGCTGGAGC
ProHisLeu LeuAspPhe LeuGluGlnLeu ThrIlePhe SerAlaSer SerArgTrpSer

1024 AACACCCGCC ACATGACCTA CTGGCGCGGC CACACCATCC AGAGCCGCCC CATCGGCGGC
AsnThrArg HisMetThr TyrTrpArgGly HisThrIle GlnSerArg ProIleGlyGly

09988462.112001

Fig. 6B

1084 GGCCTGAACA CCAGCACCCA CGGCGCCACC AACACCAGCA TCAACCCCGT GACCCTGCGC
GlyLeuAsn ThrSerThr HisGlyAlaThr AsnThrSer IleAsnPro ValThrLeuArg

1144 TTCGCCAGCC GCGACGTGTA CCGCACCGAG AGCTACGCCG GCGTGCTGCT GTGGGGCATC
PheAlaSer ArgAspVal TyrArgThrGlu SerTyrAla GlyValLeu LeuTrpGlyIle

1204 TACCTGGAGC CCATCCACGG CGTGCCCACC GTGCGCTTCA ACTTCACCAA CCCCCAGAAC
TyrLeuGlu ProIleHis GlyValProThr ValArgPhe AsnPheThr AsnProGlnAsn

1264 ATCAGCGACC GCGGCACCGC CAACTACAGC CAGCCCTACG AGAGCCCCGG CCTGCAGCTG
IleSerAsp ArgGlyThr AlaAsnTyrSer GlnProTyr GluSerPro GlyLeuGlnLeu

1324 AAGGACAGCG AGACCGAGCT GCGCCCCGAG ACCACCGAGC GCCCCAATA CGAGAGCTAC
LysAspSer GluThrGlu LeuProProGlu ThrThrGlu ArgProAsn TyrGluSerTyr

1384 AGCCACCGCC TGAGCCACAT CGGCATCATC CTGCAGAGCC GCGTGAACGT GCGCGTGTAC
SerHisArg LeuSerHis IleGlyIleIle LeuGlnSer ArgValAsn ValProValTyr

1444 AGCTGGACCC ACCGCAGCGC CGACCGCACC AACACCATCG GCCCCAACCG CATCACCCAG
SerTrpThr HisArgSer AlaAspArgThr AsnThrIle GlyProAsn ArgIleThrGln

1504 ATCCCCATGG TGAAGGCCAG CGAGCTGCCC CAGGGCACCA CCGTGGTGCG CGGCCCCGGC
IleProMet ValLysAla SerGluLeuPro GlnGlyThr ThrValVal ArgGlyProGly

1564 TTCACCGGCG GCGACATCCT GCGCCGCACC AACACCGGCG GCTTCGGCCC CATCCGCGTG
PheThrGly GlyAspIle LeuArgArgThr AsnThrGly GlyPheGly ProIleArgVal

1624 ACCGTGAACG GCCCCCTGAC CCAGCGCTAC CGCATCGGCT TCCGCTACGC CAGCACCGTG
ThrValAsn GlyProLeu ThrGlnArgTyr ArgIleGly PheArgTyr AlaSerThrVal

1684 GACTTCGACT TCTTCGTGAG CCGCGGCGGC ACCACCGTGA ACAACTTCCG CTTCTGCGC
AspPheAsp PhePheVal SerArgGlyGly ThrThrVal AsnAsnPhe ArgPheLeuArg

1744 ACCATGAACA GCGGCGACGA GCTGAAGTAC GGCAACTTCG TGCGCCGCGC CTTACCACC
ThrMetAsn SerGlyAsp GluLeuLysTyr GlyAsnPhe ValArgArg AlaPheThrThr

1804 CCCTTCACCT TCACCCAGAT CCAGGACATC ATCCGCACCA GCATCCAGGG CCTGAGCGGC
ProPheThr PheThrGln IleGlnAspIle IleArgThr SerIleGln GlyLeuSerGly

1864 AACGGCGAGG TGTACATCGA CAAGATCGAG ATCATCCCCG TGACCGCCAC CTTGAGGGC
AsnGlyGlu ValTyrIle AspLysIleGlu IleIlePro ValThrAla ThrPheGluAla

1924 GAGTACGACC TGGAGCGCGC CCAGGAGGCC GTGAACGCCC TGTTACCAA CACCAACCCC
GluTyrAsp LeuGluArg AlaGlnGluAla ValAsnAla LeuPheThr AsnThrAsnPro

1984 CGCCGCCTGA AGACCGACGT GACCGACTAC CACATCGACC AGGTGAGCAA CCTGGTGGCC
ArgArgLeu LysThrAsp ValThrAspTyr HisIleAsp GlnValSer AsnLeuValAla

2044 TGCCTGAGCG ACGAGTTCTG CCTGGACGAG AAGCGCGAGC TGCTGGAGAA GGTGAAGTAC
CysLeuSer AspGluPhe CysLeuAspGlu LysArgGlu LeuLeuGlu LysValLysTyr

Fig. 6C

2104 GCCAAGCGCC TGAGCGACGA GCGCAACCTG CTGCAGGACC CCAACTTCAC CAGCATCAAC
AlaLysArg LeuSerAsp GluArgAsnLeu LeuGlnAsp ProAsnPhe ThrSerIleAsn

2164 AAGCAGCCCG ACTTCATCAG CACCAACGAG CAGAGCAACT TCACCAGCAT CCACGAGCAG
LysGlnPro AspPheIle SerThrAsnGlu GlnSerAsn PheThrSer IleHisGluGln

2224 AGCGAGCACG GCTGGTGGGG CAGCGAGAAC ATCACCATCC AGGAGGGCAA CGACGTGTTC
SerGluHis GlyTrpTrp GlySerGluAsn IleThrIle GlnGluGly AsnAspValPhe

2284 AAGGAGAACT ACGTGACCCT GCCCGGCACC TTCAACGAGT GCTACCCAC CTACCTGTAC
LysGluAsn TyrValThr LeuProGlyThr PheAsnGlu CysTyrPro ThrTyrLeuTyr

2344 CAGAAGATCG GCGAGAGCGA GCTGAAGGCC TACACCCGCT ACCAGCTGCG CGGCTACATC
GlnLysIle GlyGluSer GluLeuLysAla TyrThrArg TyrGlnLeu ArgGlyTyrIle

2404 GAGGACAGCC AGGACCTGGA GATCTACCTG ATCCGCTACA ACGCCAAGCA CGAGACCCTG
GluAspSer GlnAspLeu GluIleTyrLeu IleArgTyr AsnAlaLys HisGluThrLeu

2464 GACGTGCCCC GCACCGAGAG CCTGTGGCCC CTGAGCGTGG AGAGCCCCAT CGGCCGCTGC
AspValPro GlyThrGlu SerLeuTrpPro LeuSerVal GluSerPro IleGlyArgCys

2524 GGCGAGCCCA ACCGCTGCGC CCCCCACTTC GAGTGGAACC CCGACCTGGA CTGCAGCTGC
GlyGluPro AsnArgCys AlaProHisPhe GluTrpAsn ProAspLeu AspCysSerCys

2584 CGCGACGGCG AGAAGTGCGC CCACCACAGC CACCACTTCA GCCTGGACAT CGACGTGGGC
ArgAspGly GluLysCys AlaHisHisSer HisHisPhe SerLeuAsp IleAspValGly

2644 TGCACCGACC TGCACGAGAA CCTGGGCGTG TGGGTGGTGT TCAAGATCAA GACCCAGGAG
CysThrAsp LeuHisGlu AsnLeuGlyVal TrpValVal PheLysIle LysThrGlnGlu

2704 GGCCACGCCC GCCTGGGCAA CCTGGAGTTC ATCGAGGAGA AGCCCCTGCT GGGCGAGGCC
GlyHisAla ArgLeuGly AsnLeuGluPhe IleGluGlu LysProLeu LeuGlyGluAla

2764 CTGAGCCGCG TGAAGCGCGC CGAGAAGAAG TGGCGCGACA AGCGCGAGAA GCTGCAGCTG
LeuSerArg ValLysArg AlaGluLysLys TrpArgAsp LysArgGlu LysLeuGlnLeu

2824 GAGACCAAGC GCGTGTACAC CGAGGCCAAG GAGGCCGTGG ACGCCCTGTT CGTGGACAGC
GluThrLys ArgValTyr ThrGluAlaLys GluAlaVal AspAlaLeu PheValAspSer

2884 CAGTACGACC GCCTGCAGGC CGACACCAAC ATCGGCATGA TCCACGCCGC CGACAAGCTG
GlnTyrAsp ArgLeuGln AlaAspThrAsn IleGlyMet IleHisAla AlaAspLysLeu

2944 GTGCACCGCA TCCGCGAGGC CTACCTGAGC GAGCTGCCCG TGATCCCCGG CGTGAACGCC
ValHisArg IleArgGlu AlaTyrLeuSer GluLeuPro ValIlePro GlyValAsnAla

3004 GAGATCTTCG AGGAGCTGGA GGGCCACATC ATCACCGCCA TCAGCCTGTA CGACGCCCGC
GluIlePhe GluGluLeu GluGlyHisIle IleThrAla IleSerLeu TyrAspAlaArg

Fig. 6D

3064 AACGTGGTGA AGAACGGCGA CTTCAACAAC GGCCTGACCT GCTGGAACGT GAAGGGCCAC
 AsnValVal LysAsnGly AspPheAsnAsn GlyLeuThr CysTrpAsn ValLysGlyHis
 3124 GTGGACGTGC AGCAGAGCCA CCACCGCAGC GACCTGGTGA TCCCCGAGTG GGAGGCCGAG
 ValAspVal GlnGlnSer HisHisArgSer AspLeuVal IleProGlu TrpGluAlaGlu
 3184 GTGAGCCAGG CCGTGCGCGT GTGCCCCGGC TCGGGCTACA TCCTGCGCGT GACCGCCTAC
 ValSerGln AlaValArg ValCysProGly CysGlyTyr IleLeuArg ValThrAlaTyr
 3244 AAGGAGGGCT ACGGCGAGGG CTGCGTGACC ATCCACGAGA TCGAGAACAA CACCGACGAG
 LysGluGly TyrGlyGlu GlyCysValThr IleHisGlu IleGluAsn AsnThrAspGlu
 3304 CTGAAGTTCA AGAACGGCGA GGAGGAGGAG GTGTACCCCA CCGACACCGG CACCTGCAAC
 LeuLysPhe LysAsnArg GluGluGluGlu ValTyrPro ThrAspThr GlyThrCysAsn
 3364 GACTACACCG CCCACCAGGG CACCGCCGGC TCGCGCGACG CCTGCAACAG CCGCAACGCC
 AspTyrThr AlaHisGln GlyThrAlaGly CysAlaAsp AlaCysAsn SerArgAsnAla
 3424 GGCTACGAGG ACGCCTACGA GGTGGACACC ACCGCCAGCG TGAAC TACAA GCCCACCTAC
 GlyTyrGlu AspAlaTyr GluValAspThr ThrAlaSer ValAsnTyr LysProThrTyr
 3484 GAGGAGGAGA CCTACACCGA CGTGCGCCGC GACAACCACT GCGAGTACGA CCGCGGCTAC
 GluGluGlu ThrTyrThr AspValArgArg AspAsnHis CysGluTyr AspArgGlyTyr
 3544 GTGAACTACC CCCCCGTGCC CGCCGGCTAC GTGACCAAGG AGCTGGAGTA CTTCCCCGAG
 ValAsnTyr ProProVal ProAlaGlyTyr ValThrLys GluLeuGlu TyrPheProGlu
 3604 ACCGACACCG TGTGGATCGA GATCGGCGAG ACCGAGGGCA AGTTCATCGT GGACAGCGTG
 ThrAspThr ValTrpIle GluIleGlyGlu ThrGluGly LysPheIle ValAspSerVal
 3664 GAGCTGCTGC TGATGGAGGA GTAG
 GluLeuLeu LeuMetGlu Glu---

09938462-112001

Fig. 7A

SEQUENCE OF THE FULL-LENGTH HYBRID SYNTHETIC/NATIVE CRYIA(B) CHIMERIC GENE
The fusion point between the synthetic and native coding sequences is indicated by a slash (/) in the sequence.

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu
61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu
121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCCGCG CCGGCTTCGT GCTGGGCCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu
181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle
241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu
301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp
361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla
421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal
481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln
541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle
601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly
661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal
721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal
781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe
841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu
901 AACAGCATCA CCATCTACAC CGACGCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

Fig. 7B

961 ATCATGGCCA GCCCGTCGG CTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCAGCA TCCCCCTGAC CAAGAGCACC
GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCAGC CCCCCTGAGC
ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

0988462-112001

Fig. 7C

1921 ACCGACTACC ACATCGAT/CA AGTATCCAAT TTAGTTGAGT GTTTATCTGATGAATTTTGT
ThrAspTyr HisIleAsp/GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

2041 CGGAATTTAC TTCAAGATCC AAACCTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGAA AATGTGCCCA TCATTCCCAT
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysAla HisHisSerHis

2401 CATTTCTCCT TGGACATTGA TGTTGGATGT ACAGACTTAA ATGAGGACTT AGGTGTATGG
HisPheSer LeuAspIle AspValGlyCys ThrAspLeu AsnGluAsp LeuGlyValTrp

2461 GTGATATTCA AGATTAAAGAC GCAAGATGGC CATGCAAGAC TAGGAAATCT AGAATTTCTC
ValIlePhe LysIleLys ThrGlnAspGly HisAlaArg LeuGlyAsn LeuGluPheLeu

2521 GAAGAGAAAC CATTAGTAGG AGAAGCACTA GCTCGTGTGA AAAGAGCGGA GAAAAAATGG
GluGluLys ProLeuVal GlyGluAlaLeu AlaArgVal LysArgAla GluLysLysTrp

2581 AGAGACAAAC GTGAAAAATT GGAATGGGAA ACAAATATTG TTTATAAAGA GGCAAAAGAA
ArgAspLys ArgGluLys LeuGluTrpGlu ThrAsnIle ValTyrLys GluAlaLysGlu

2641 TCTGTAGATG CTTTATTTGT AAACCTCTCAA TATGATAGAT TACAAGCGGA TACCAACATC
SerValAsp AlaLeuPhe ValAsnSerGln TyrAspArg LeuGlnAla AspThrAsnIle

2701 GCGATGATTC ATGCGGCAGA TAAACGCGTT CATAGCATTG GAGAAGCTTA TCTGCCTGAG
Ala e Ile HisAlaAla AspLysArgVal HisSerIle ArgGluAla TyrLeuProGlu

2761 CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTGAAG AATTAGAAGG GCGTATTTTC
LeuSerVal IleProGly ValAsnAlaAla IlePheGlu GluLeuGlu GlyArgIlePhe

2821 ACTGCATTCT CCCTATATGA TGCGAGAAAT GTCATTAAAA ATGGTGATTT TAATAATGGC
ThrAlaPhe SerLeuTyr AspAlaArgAsn ValIleLys AsnGlyAsp PheAsnAsnGly

09083452-112001

Fig. 7D

2881 TTATCCTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTCC
LeuSerCys TrpAsnVal LysGlyHisVal AspValGlu GluGlnAsn AsnHisArgSer

2941 GTCCTTGTTG TTCCGGAATG GGAAGCAGAA GTGTCACAAG AAGTTCGTGT CTGTCCGGGT
ValLeuVal ValProGlu TrpGluAlaGlu ValSerGln GluValArg ValCysProGly

3001 CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC
ArgGlyTyr IleLeuArg ValThrAlaTyr LysGluGly TyrGlyGlu GlyCysValThr

3061 ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA
IleHisGlu IleGluAsn AsnThrAspGlu LeuLysPhe SerAsnCys ValGluGluGlu

3121 GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG
ValTyrPro AsnAsnThr ValThrCysAsn AspTyrThr AlaThrGln GluGluTyrGlu

3181 GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA
GlyThrTyr ThrSerArg AsnArgGlyTyr AspGlyAla TyrGluSer AsnSerSerVal

3241 CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT
ProAlaAsp TyrAlaSer AlaTyrGluGlu LysAlaTyr ThrAspGly ArgArgAspAsn

3301 CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA
ProCysGlu SerAsnArg GlyTyrGlyAsp TyrThrPro LeuProAla GlyTyrValThr

3361 AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA
LysGluLeu GluTyrPhe ProGluThrAsp LysValTrp IleGluIle GlyGluThrGlu

3421 GGAACATTCA TCGTGGACAG CGTGGAATTA CTTCTTATGG AGGAATAA
GlyThrPhe IleValAsp SerValGluLeu LeuLeuMet GluGlu---

0998462.1.2001

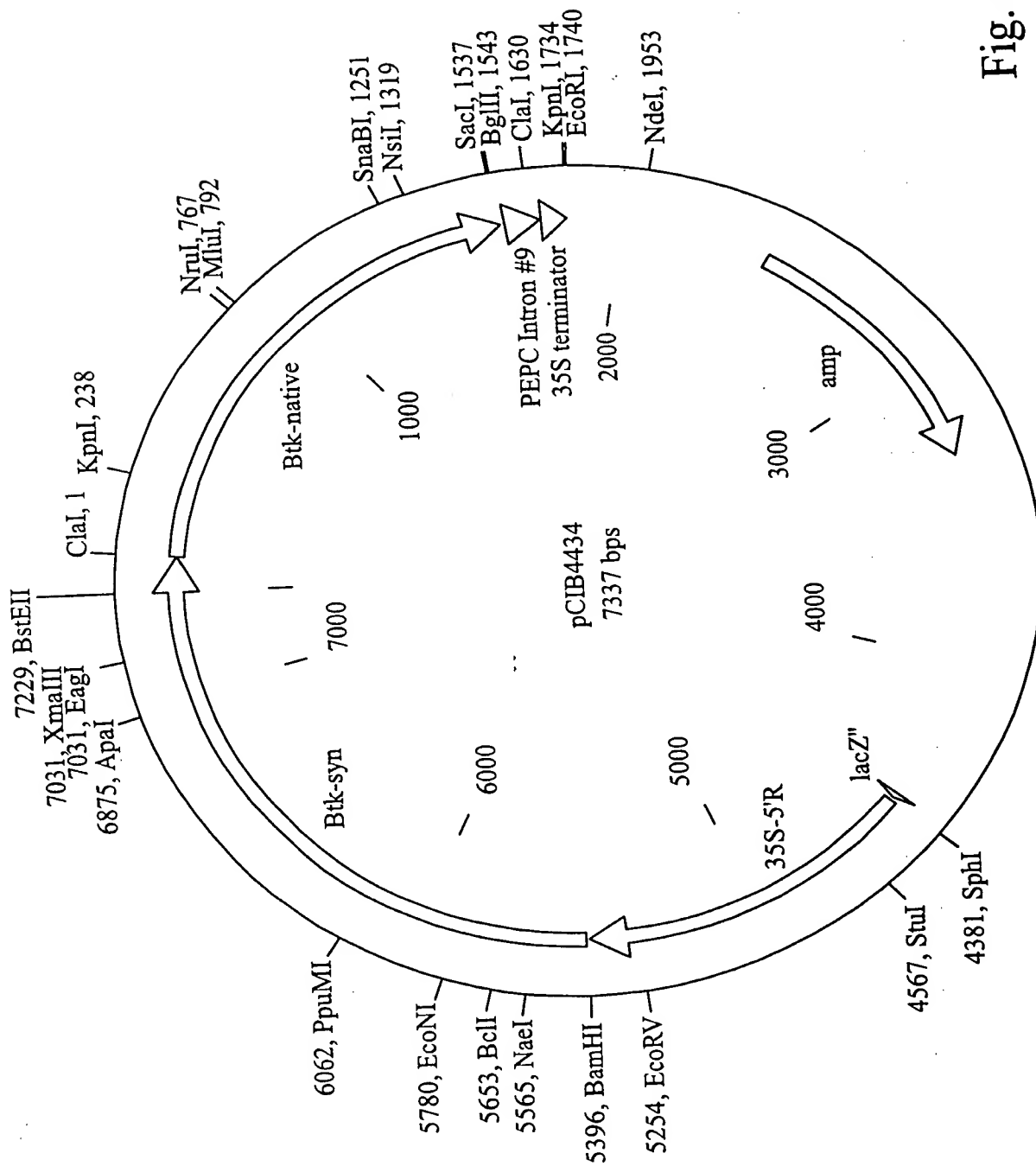


Fig. 8

Fig. 9A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCCGCG CCGGCTTCGT GCTGGGCCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

09988462.1.2001

Fig. 9B

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCGA CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACC GC CCCCTGAGC
ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCAACA ACCTGCAGTT CCACACCAGC
GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT
ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

0988462-12001

Fig. 9C

2041 CGGAATTTAC TTCAAGATCC AAACCTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGCAGCCTGT GGCCCTGAG CGCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCTCAT GCGGCAGATA AACGCGTTCA TAGCATTCTGA
GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTCCGT CCTTGTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

Fig. 9D

3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGGATTA CACACCACTA
AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGAG AAACGGAAGG AACATTATC GTGGACAGCG TGGAATTACT TCTTATGGAG
GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAATAA
Glu---

0998462 112001

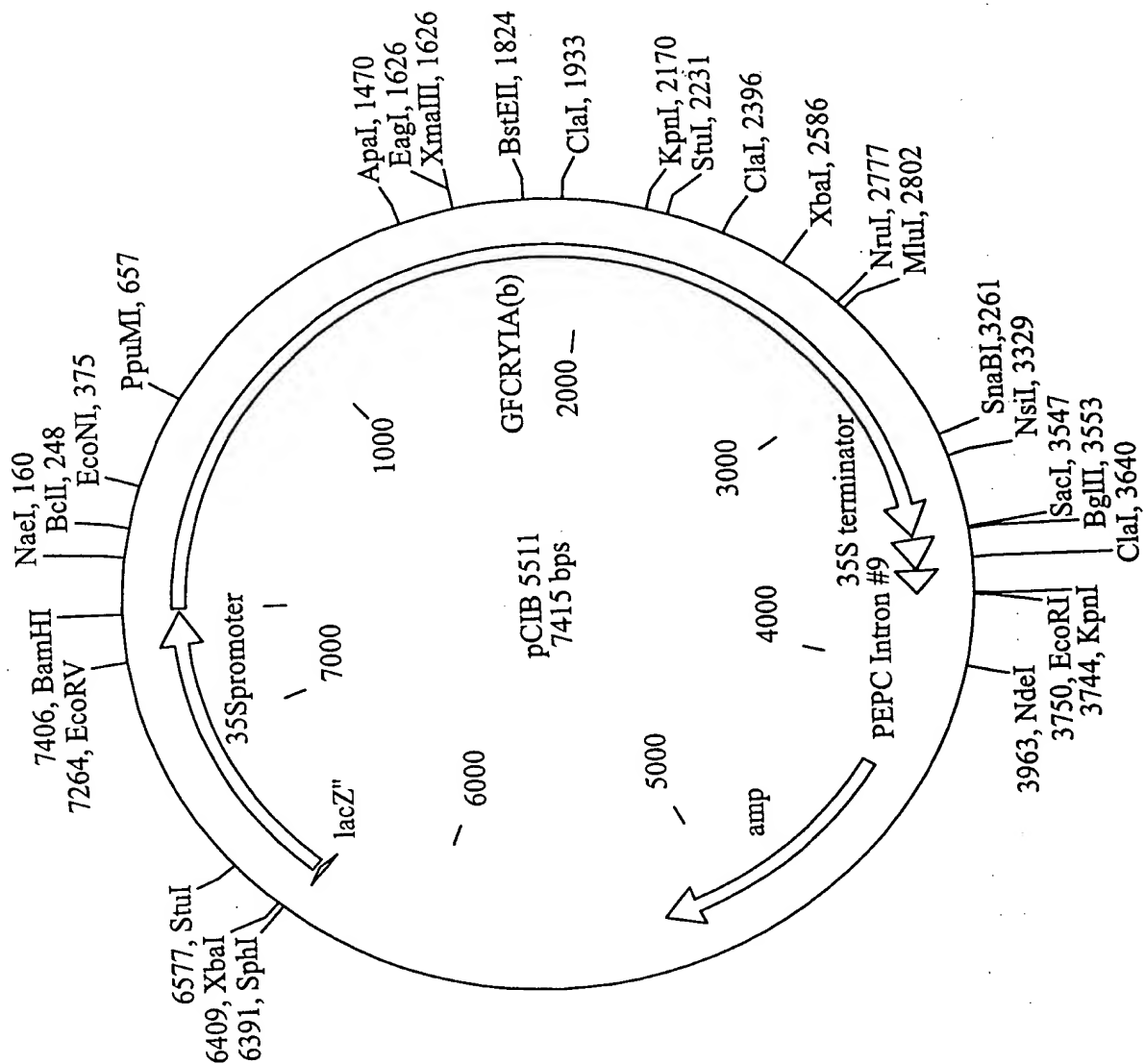


Fig. 10

Fig. 11A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCCGCG CCGGCTTCGT GCTGGGCGCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCGCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCTT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

09988462-112001

Fig. 11B

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCAGCA TCCCCCTGAC CAAGAGCACC
GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCGA CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GCTTAAGCGA CGAGTTCTGC
ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG
LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

000046-12001

Fig. 11C

2041 CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCGACGACG TGTTCAAGGA GAACTACGTG
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCACC ACAGCCACCA CTTAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA
GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTCCGGT CTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

Fig. 11D

3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA CAGACGAACT GAAGTTTAGC
GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGAG AAACGGAAGG AACATTATC GTGGACAGCG TGGAATTACT TCTTATGGAG
GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAATAA
Glu---

00000462-112001

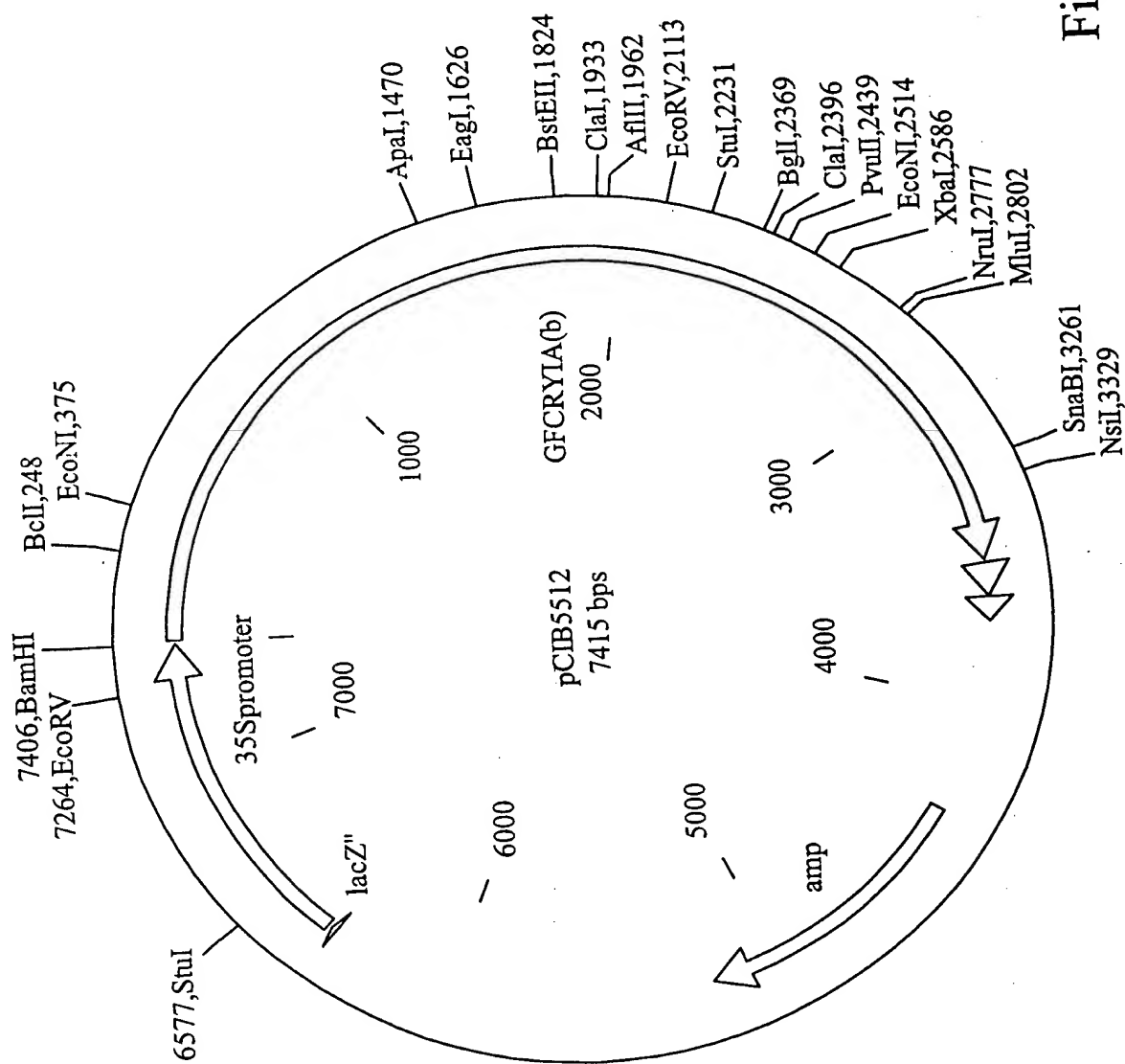


Fig. 12

Fig. 13A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCCGCG CCGGCTTCGT GCTGGGCCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCTT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCGTCTGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

098462-12001

Fig. 13B

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCAGCA TCCCCCTGAC CAAGAGCACC
GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCGA CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CTTCAACTT CAGCAACGGC
LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GCTTAAGCGA CGAGTTCTGC
ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG
LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

0998462 112001

Fig. 13C

2041 CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCAGACGACG TGTTCAGGA GAACTACGTG
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCACC ACAGCCACCA CTTAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGCAATCTAG AGTTCCTGGA GGAGAAGCCC CTGGTGGGCG AGGCCCTGGC CCGCGTGAAG
GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641 CGCGCCGAGA AGAAGTGGCG CGACAAGCGC GAGAAGCTGG AGTGGGAGAC CAACATCGTG
ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TACAAGGAGG CCAAGGAGAG CGTGGACGCC CTGTTCGTGA ACAGCCAGTA CGACCGCCTG
TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAGGCCGACA CCAACATCGC CATGATCCAC GCCGCCGACA AGCGCGTGCA CAGCATTTCG
GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAGGCCTACC TGCCCGAGCT GAGCGTGATC CCCGGCGTGA ACGCCGCCAT CTTTCGAGGAA
GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 CTCGAGGGCC GCATCTTCAC CGCCTTCAGC CTGTACGACG CCCGCAACGT GATCAAGAAC
LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGCGACTTCA ACAACGGCCT GAGCTGCTGG AACGTGAAGG GCCACGTGGA CGTGGAGGAG
GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAGAACAACC ACCGCAGCGT GCTGGTGGTG CCCGAGTGGG AGGCCGAGGT GAGCCAGGAG
GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

Fig. 13D

3061 GTGCGCGTGT GCCCCGGCCG CGGCTACATC CTGCGCGTGA CCGCCTACAA GGAGGGCTAC
ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGCGAGGGCT GCGTGACCAT CCACGAGATC GAGAACAACA CCGACGAGCT CAAGTTCAGC
GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGCGTGG AGGAGGAGGT GTACCCCAAC AACACCGTGA CCTGCAACGA CTACACCGCG
AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACCCAGGAGG AGTACGAGGG CACCTACACC AGCCGCAACC GCGGCTACGA CGGCGCCTAC
ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAGAGCAACA GCAGCGTGCC CGCCGACTAC GCCAGCGCCT ACGAGGAGAA GGCCTACACC
GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GACGGCCGCC GCGACAACCC CTGCGAGAGC AACCGCGGCT ACGGCGACTA CACCCCCCTG
AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCCGCCGGCT ACGTGACCAA GGAGCTGGAG TACTTCCCCG AGACCGACAA GGTGTGGATC
ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGCG AGACCGAGGG CACCTTCATC GTGGACAGCG TGGAGCTGCT GCTGATGGAG
GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAG
Glu

0908462-12001

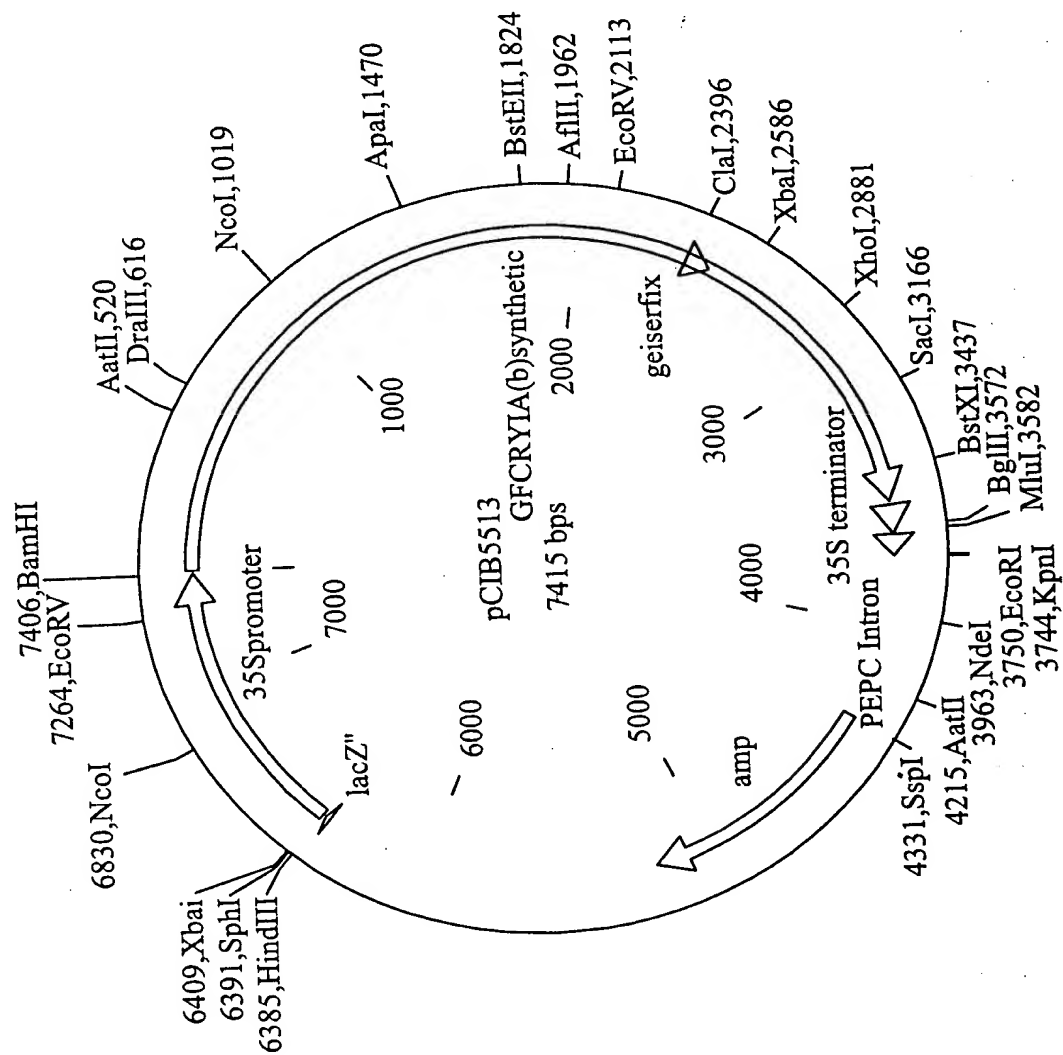


Fig. 14

Fig. 15A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCCGCG CCGGCTTCGT GCTGGGCCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

09864-1

1021	ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGATCCG MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
1081	ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu
1141	AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal
1201	TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal
1261	CCACCTCGAC AGGGCTTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe
1321	AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla
1381	GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr
1441	AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu
1501	CGCCGCACCA GCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer
1561	CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCAcca ACCTGCAGTT CCACACCAGC GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer
1621	ATCGACGGCC GCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn
1681	CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly
1741	AGCAGCGTGT TCACCCTGAG CGCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp
1801	CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla
1861	CAGAAGGCCG TGAACGAGCT GTTACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal
1921	ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys
1981	CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

Fig. 15C

2041 CGGAATTTAC TTCAAGATCC AAACCTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 TTAGAAATCT ATTTAATTTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGCA AGTGCGGGGA GCCGAATCGA
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCACC ACAGCCACCA CTTACGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TG TAGATGCT TTATTGTAA ACTCTCAATA TGATAGATTA
TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCTGA
GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TG TAGAAGAA
GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

0908462-112001

Fig. 15D

3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
 ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr
 3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
 GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer
 3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
 AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla
 3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
 ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr
 3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
 GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr
 3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
 AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu
 3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
 ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle
 3481 GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
 GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu
 3541 GAATAAG
 Glu---

09983462-112001

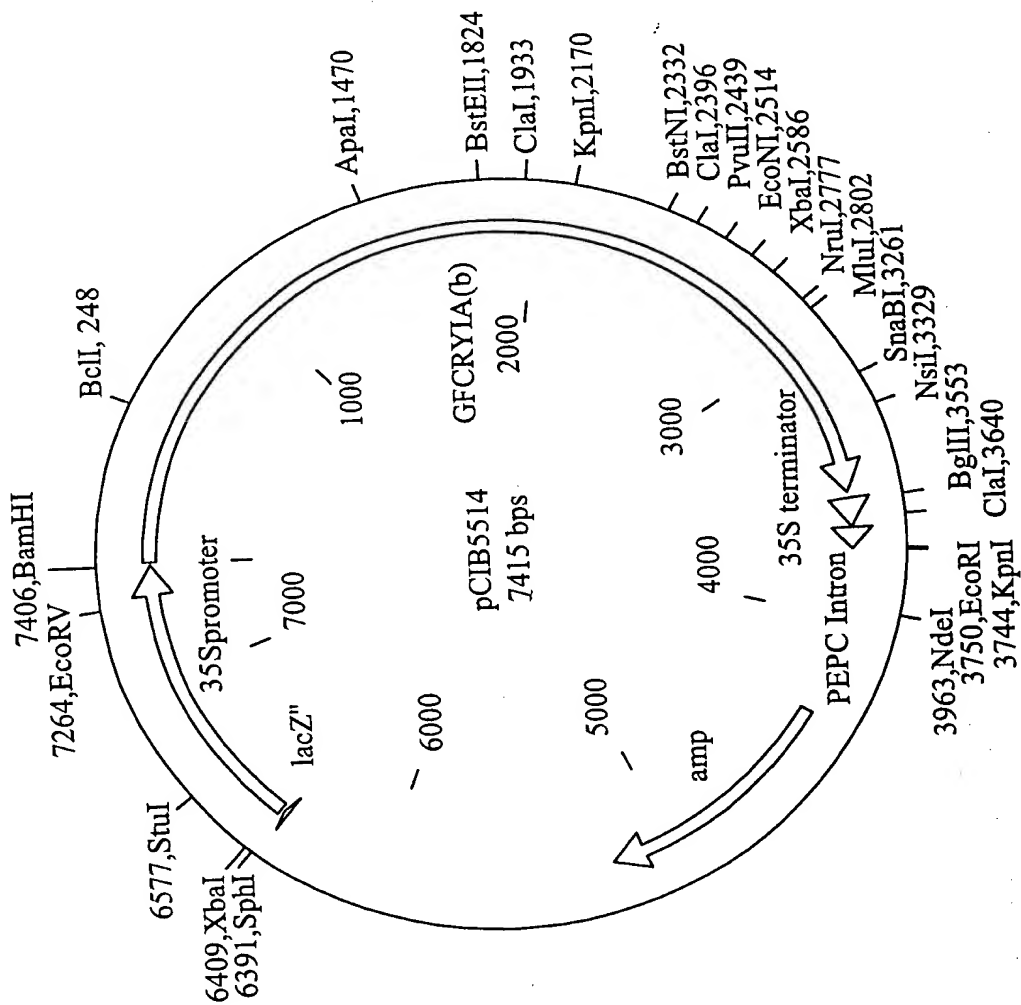


Fig. 16

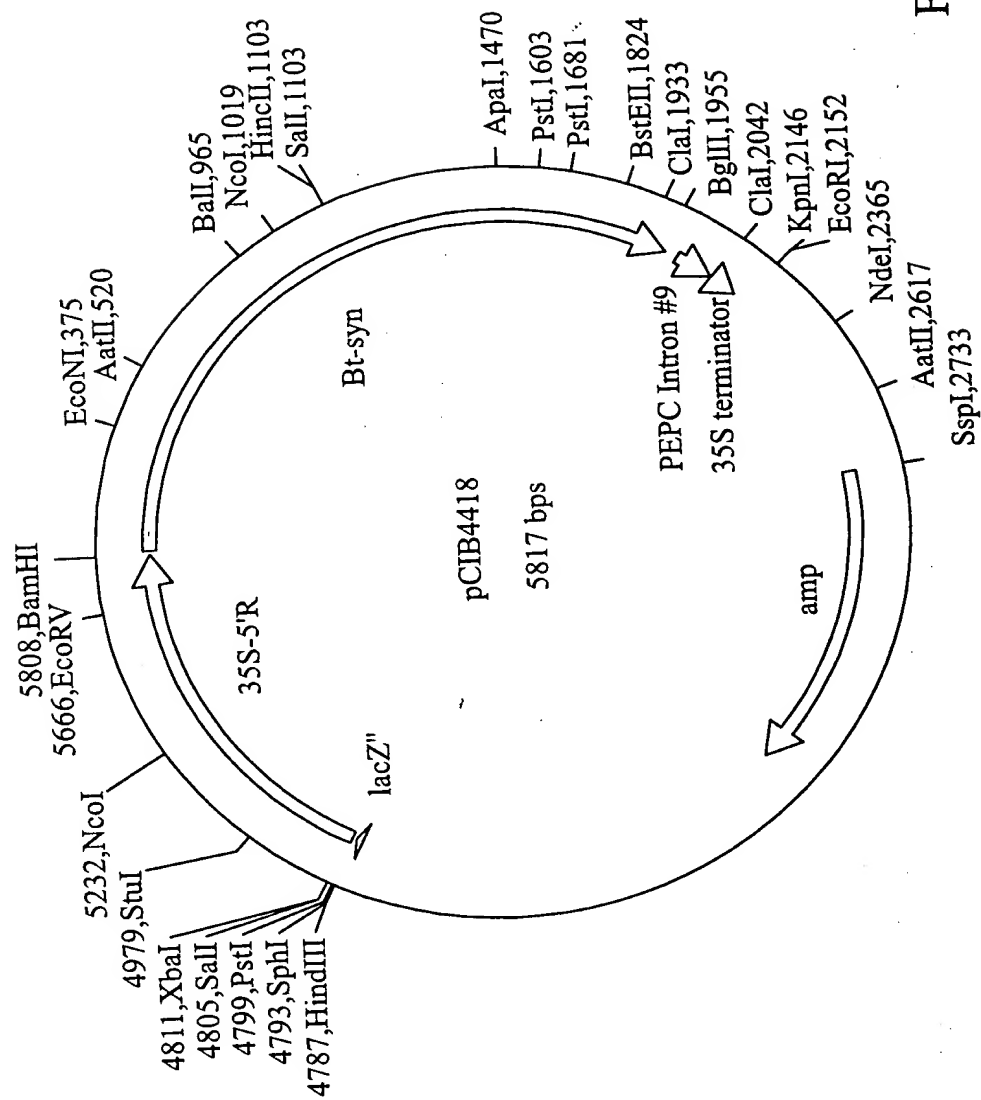


Fig. 17

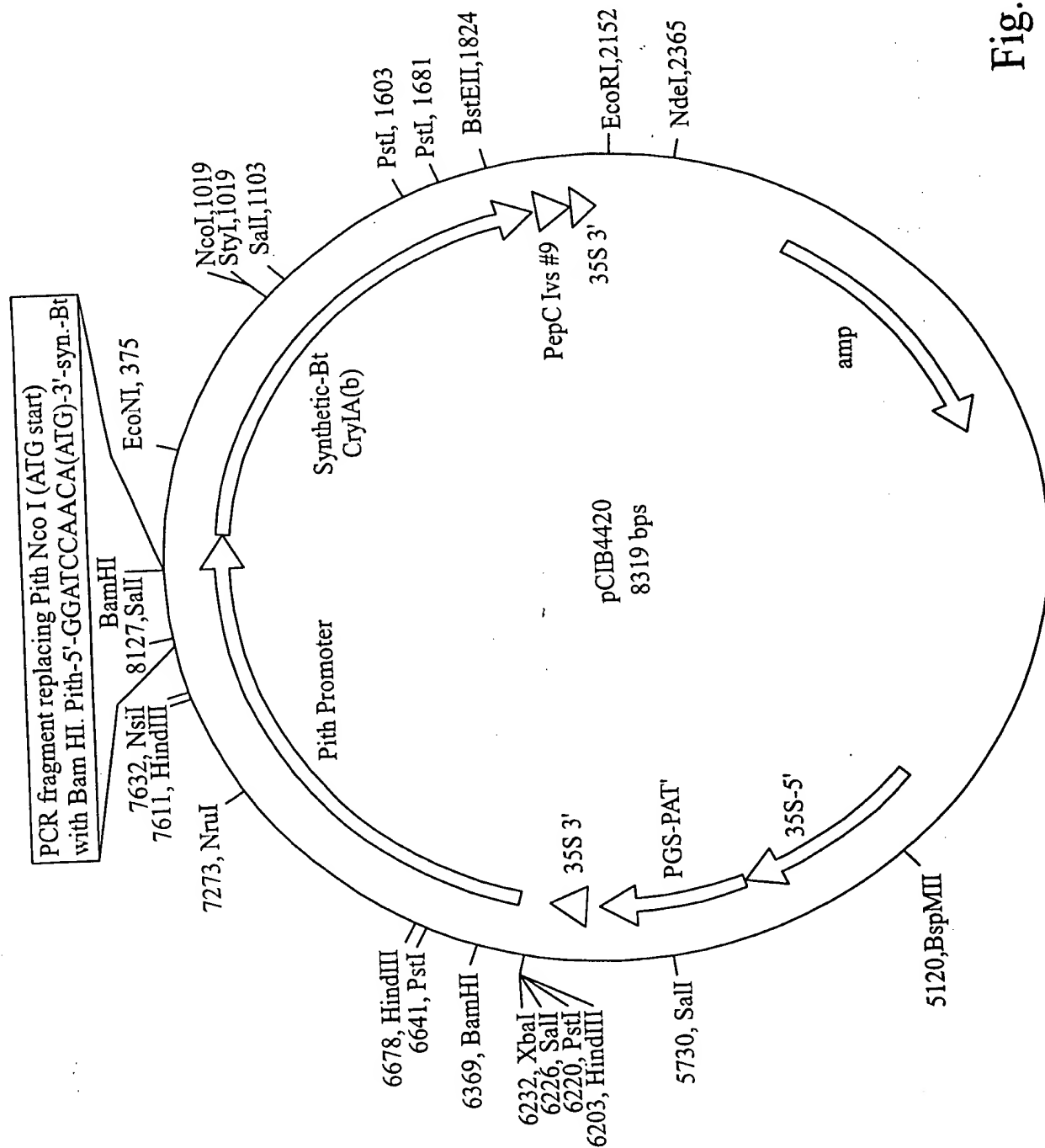


Fig. 18

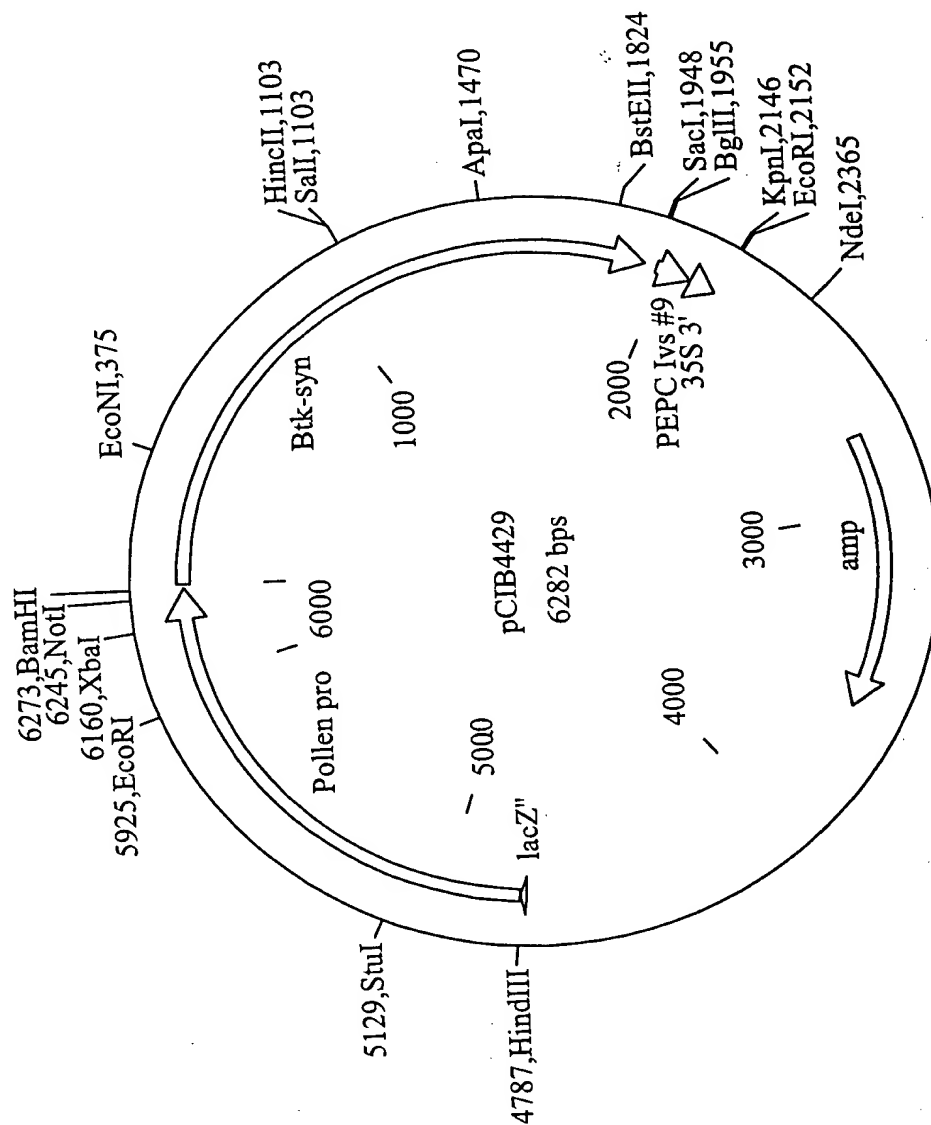


FIG. 19

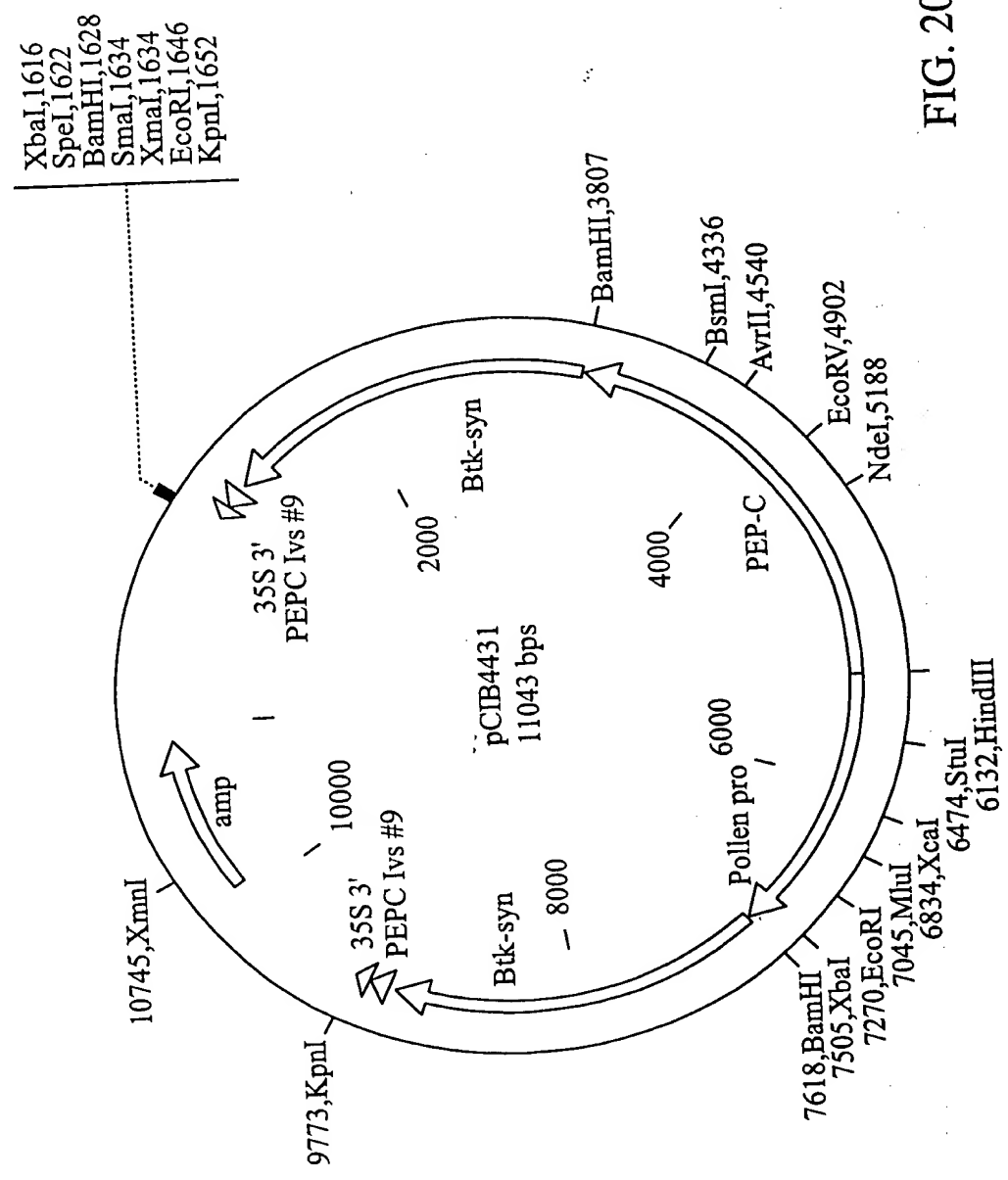


FIG. 20

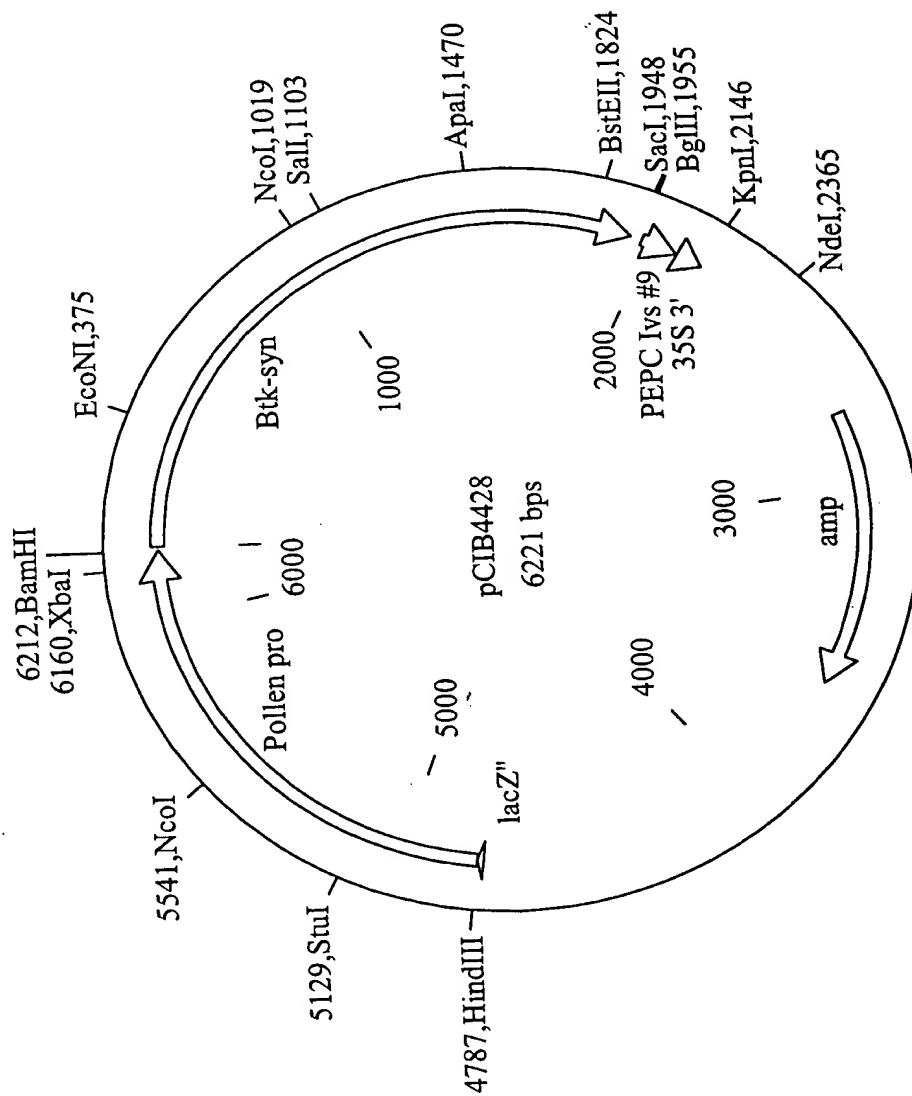


FIG. 21

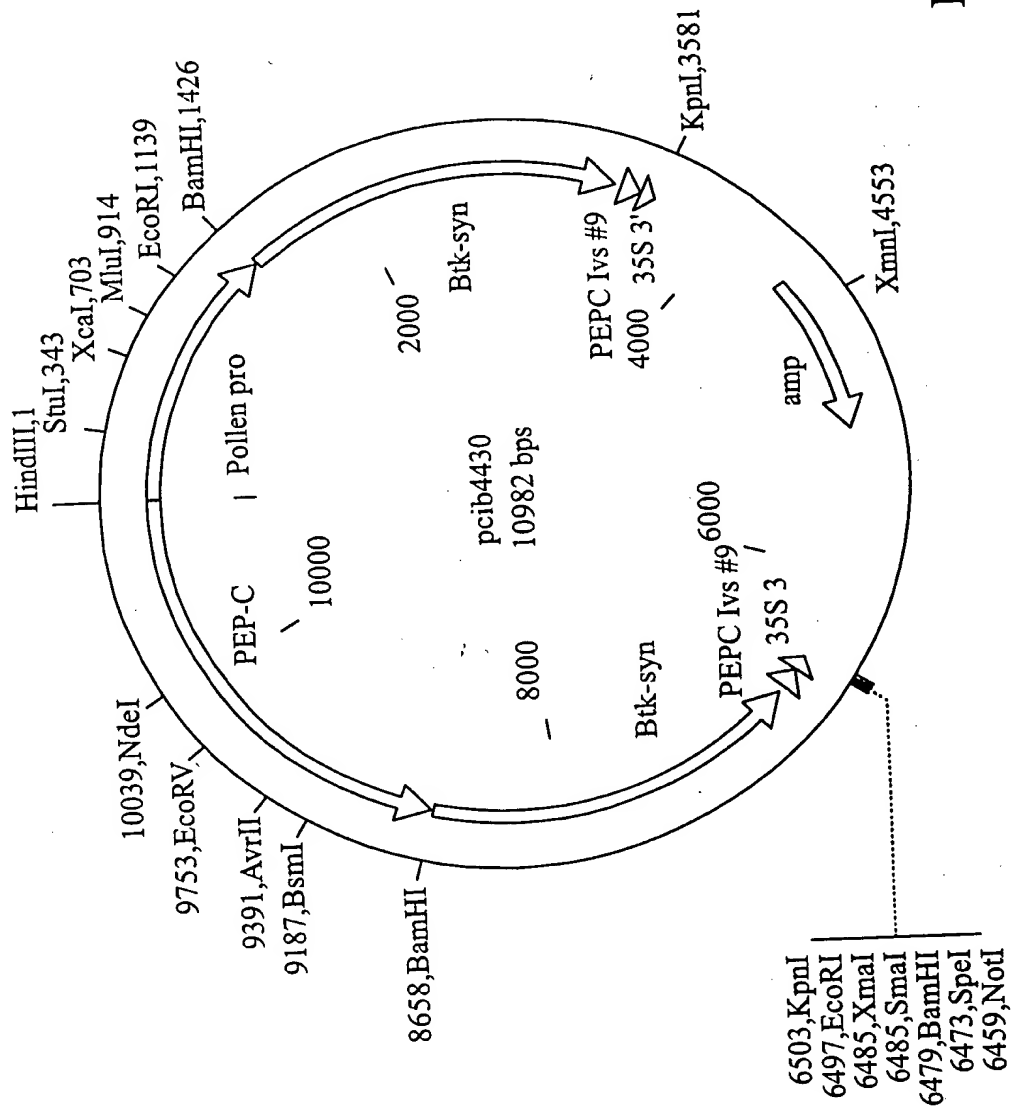


FIG. 22

Fig. 23A

CryIA(b) Protein Levels in Transgenic Maize

ELISA Bt Values of Field Plants:

INBRED X PARENT	ABRU PLANT Number	ng Bt/mg protein
2ND01X171-4A	1646	29
5N984X171-4A	857	1705
5N984X171-4A	870	1760
5N984X171-13	969	22
5N984X171-15	1468	17
5N984X171-15	1470	28
5N984X171-15	1502	180
5N984X171-14A	1529	1500
5N984X171-14A	1667	408
5N984X176-11	1671	1270
5N984X176-11	1673	1522
5N984X176-11	1675	943
5N984X176-11	1679	967
5N984X176-11	1942	15
5N984X171-4B	1946	16
5N984X171-4B	1101	30
5NA56X171-16ABX	1622	959
5NA89X176-11	1630	1172
5NA89X176-11	1635	1100
5NA89X176-11	825	103
6F010X171-4	832	1298
6F010X171-4		

-Bt levels are in ng cryIA(b)/mg total protein.

-Data are from progeny of the described maize transformants expressing the cryIA(b) protein.

-ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

09983462-112001

Fig. 23B

Bioassay of European corn borer, *Ostrinia nubilalis*, and sugarcane borer, *Diatraea saccharalis*

Plasmid	Promoter	Cross	Plant No.	Bt Gene	Percent Mortality	
					Ostrinia	Diatraea
pCIB4431	PEPC	5N984 X 176-8B	21	+	100	100
			22	-	0	0
			40	+	100	100
pCIB4431	PEPC	5N984 X 176-11	95	+	100	100
			96	-	0	0
			98	+	100	100
pCIB4418	35S	5N984 X 171-14A	45	-	0	10
			64	+	100	90
			68	+	100	100
pCIB4431	PEPC	2N217AF X 176-8B	1	-	0	0
			3	+	100	100
			4	+	100	100
pCIB4418	35S	2N217AF X 171-15	70	-	10	0
			83	+	90	80
			88	+	90	100

Fig. 23C

CryIA(b) Protein Levels in Transgenic Maize

Greenhouse plants

35S LINE	LEAF	PITH	ROOT	POLLEN
6F010 x 171-4A	-409 + 288	NT	NT	NT
5N984 x 171-14A	256 + 159	191	198	30
6F010 x 171-16AB	240 + 174	221	271	NT
5N984 x 171-13	201 + 94	NT	NT	NT
5NA89 x 171-13	37 + 7	150	0	NT
5N984 x 171-18	7.7 + 3	NT	NT	NT
6N615 x 171-16AB	7.5 + 3	0	0	
PEPC LINE				
6N615 x 176-11	1126 + 419	41	19	NT
6F010 x 176-10	774 + 159	NT	NT	130
5N984 x 176-11	719 + 128	16	20	186

-Bt levels are in ng cryIA(b)/mg total protein.

Data are from progeny of the described maize transformants expressing the cryIA(b) protein.

ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

Fig. 23D

Bioassay of European corn borer, *Ostrinia nubilalis*, on Pith:SynBt maize

Plasmid	Promoter	Event	Plant No.	Percent Mortality
pCIB4433	Pith	JS21A-Top	1	90
			3	80
			11	90
			13	70
			14	75
			19	85
			28	80
pCIB4433	Pith	JS22D-Mid	3	70
			4	65
			7	85
			17	95
			1	5
			2	0
			3	0
		Control		

Fig. 23E

EXPRESSION OF THE CRYIA(b) GENE IN TRANSGENIC MAIZE USING THE PITH-PREFERRED PROMOTER

Leaf samples from small plantlets transformed with pCIB4433 using procedures described elsewhere were analyzed for the presence of the cryIA(b) protein using ELISA. All plants expressing cryIA(b) were found to be insecticidal in the standard European corn borer bioassay.

Note that the pith-preferred promoter has a low, but detectable level of expression in leaf tissue of maize. Detection of CryIA(b) protein is consistent with this pattern of expression.

PLANT NUMBER	ng cryIA(b)/mg protein
JS21A-1 TOP	169
JS21A-2 TOP	0
JS21A-3 TOP	113
JS21A-11 TOP	127
JS21A-12 TOP	112
JS21A-13 TOP	97
JS21A-14 TOP	118
JS21A-19 TOP	82
JS21A-24 TOP	0
JS21A-28 TOP	154
JS22D-3 MID	2946
JS22D-4 MID	5590
JS22D-11 MID	215
JS22D-17 MID	3004

Fig. 24A

1 GAATTCGGATCCATTAAAGAAGTCTTTGAACAGATTCTAGAGATCTAGTTTAATGAGCTC 60
61 CCAAAAGTCTTGAAAAAATTCAGCGGGGAGGCCATTAGGGCAGGGGTACTGTTATGTTTT 120
121 AAAGAGAACACCACTTTCTTGATCTCTTCTAAAGAGAAATGTTTTGTAAGAAGGATCCTG 180
181 TCCTCCTCATCCAACCTTTTCATCGGCAAATTTTTCATAGAGATATTAGAGGCAAGAGAG 240
241 GGGCCAAAAGATCCATGTAAATGGAAGTGGCCACCTGGTTGATACCTCCCTCATCTTCA 300
301 ACAGAAAATCCATTATGAAAAAGTGAATGGATTTTAAACTCTTCTTTTTCTTCCCTTTTG 360
361 CAATGAGCTGAAAAATATCTGGTATTATTCTCATCACCCCTCATTAATGAATCTGTCCCTAG 420
421 CAATTTGCTTTTCTCTTGATCCCTTCTGCAGCCACCATGTTTCTTAAATTCCACTCCATAT 480
481 CAAGCTTTTCCAATCTATCAGAATCTGAGATGGCTGCAATCTCTCTCATTTTCTCAAGGA 540
541 TATCGATGTTATCCATAAGGTATTTCTTGAACCTTCTTATATTTCCCTTCGACATTTATAT 600
601 TCCATCCTTTCAACATTTTGTGTTCAATCTTTTTTGTGTTTTTCCCTTTCCAAACATCGA 660
661 TACATTTCTGCTCCTCACAGGTAAGGACGAGCTTTCAAAAAACCTTCTGCTTTAAAGTC 720
721 AGGTCTGAGCCTCCAGCAAAGCTCACATATCTAAAGTCCCTCTTCTTAGTTGGGACAGAG 780
781 TCAGTGCTAAGACACATGGGAACATGACCAGAAAAAATCATATTTAGCCACAGAGAC 840
841 AACAAATATTCTTGACTGCAAGTCTCGTTATGGGCTAGCAAAGGAATCTACCCAACTTCT 900
901 CAAATGTGTTGGGATGTCAAGTATATAGACTATTATCATGTTCCAACCTATCAAACGT 960
961 GCAGCTCAATTATAGAGTTGAATAAAGTGCTCCATCTATTTGTTCTTATCCTCATATTTG 1020
1021 GTTAAGATATTAATAACCTCCCACCAACATTTAAAGTGCACCATTAAAGTGGCTCGC 1080
1081 GAGCACCAAACCGCTGAAAACCGGAAATGTTTAGCACGTTGGCAGCGGGACCCTTTTCTA 1140
1141 TCTCATCGTGTCTTCTGTTGTCCACCACGGCCACGGGCCAACGCTCCTCCATCCTGTAG 1200
1201 TGTAGAGTATATTCCATTTGCGACCGAGCCGAGCATCGATCCAGCCACACTGGCCACTGC 1260
1261 CAGCCAGCCATGTGGCACTCCTACGTATACTACGTGAGGTGAGATTCACTCACATQGGAT 1320
-465 -405
1321 GGGACCGAGATATTTTACTGCTGTGGTTGTGTGAGAGATAATAAAGCATTATGACGATT 1380
1381 GCTGAACAGCACACCATGCGTCCAGATAGAGAAAGCTTTCTCTCTTTATTCGCATGCA 1440
1441 TGTTTCATTATCTTTTATCATATATATATAACACATATTAAATGATTCTTCGTTCCAATT 1500
-285 -226
1501 TATAATTCATTTGACTTTTTTATCCACCGATGCTCGTTTTATTAAAAAAATATTATAAT 1560
-225 -166
1561 TATTGTTACTTTTTTGTGTAATATTGTTTAGCATATAATAAACTTTGATACTAGTATGTT 1620
-165 -106
1621 TCCGAGCAAAAAAATATTAATATTTAGATTACGAGCCCATTAATTAATTATATTCGAG 1680
-105 -46
1681 ACAAGCGAAGCAAAGCAAAGCAAGCTAATGTTGCCCTGCTGTGCATGCAGAGGCCCGCT 1740
-45 +15
1741 CTTGCTATAAACGAGGCAGCTAGACGCGACTCGACTCATCAGCCTCATCAACCTCGACGA 1800
+16 +75
1801 AGGAGGAACGAACGGACAGGTTGTTGCACAGAAGCGACATGGCTTTTCGCGCCCAAAACGT 1860
+76 M A F A P K T S +135

Fig. 24B

1861 CCTCCTCCTCCTCGCTGTCTCGGCGTTGCAGGCAGCTCAGTCGCCGCCGCTGCTCCTGA 1920
+126 S S S S L S S A L Q A A Q S P P L L L R +195

1921 GCGGATGTCGTCGACCGCAACACCGAGACGGAGGTACGACGCGGCCGTCGTCGTCACCTA 1980
+196 R M S S T A T P R R R Y D A A V V V T T +255

1981 CCACCACCACTGCTAGAGCTGCGGCGGCTGCTGTACGGTTCGCGCGCCCGCCGCGCAGG 2040
+256 T T T A R A A A A A V T V P A A P P Q A +315

2041 CGGGCCGCCGCCGCCGGTGCCACCAAAGCAAGCGGCGGCCACCGCAGAGGAGGAGCCGTC 2100
+316 G R R R R C H Q S K R R H P Q R R S R P +375

2101 CGGTGTGCGACACCATGGCGGCGCTCATGGCCAAGGGCAAGGTTCTGTATAGTACGCGCGC 2160
+376 V S D T M A A L M A K G K

2161 GTGTCGTCGTCGTTATTTTGCGCATAGGCGCGGACATACACGTGCTTTAGCTAGCTAACA 2220
2221 GCTAGATCATCGGTGCAGACGGCGTTCATCCCGTACATCACC GCCGCGGACCCGACCTA 2280
T A F I P Y I T A G D P D L

2281 GCGACGACGGCCGAGGCGCTGCGTCTGCTGGACGGCTGTGGCGCCGACGTCATCGAGCTG 2340
A T T A E A L R L L D G C G A D V I E L

2341 GGGGTACCCTGCTCGGACCCCTACATCGACGGGCCCCATCATCCAGGCGTCGGTGGCGCGG 2400
G V P C S D P Y I D G P I I Q A S V A R

2401 GCTCTGGCCAGCGGCACCACCATGGACGCCGTGCTGGAGATGCTGAGGGAGGTGACGCCG 2460
A L A S G T T M D A V L E M L R E V T P

2461 GAGCTGTCTGTCGCCCCGTGGTGCTCCTCTCCTACTACAAGCCCATCATGTCTCGCAGCTTG 2520
E L S C P V V L L S Y Y K P I M S R S L

2521 GCCGAGATGAAAGAGGCGGGGTCCACGGTAAGTATAGCTAGCTCTTCCGATCCCCCTTC 2580
A E M K E A G V H

2581 AATTAATTAATTTATAGTAGTCCATTTCATGTGATGATTTTGTCTTTTCTTTTACTGACA 2640
2641 GGTCTTATAGTGCCTGATCTCCCGTACGTGGCCGCGCACTCGCTGTGGAGTGAAGCCAAG 2700
G L I V P D L P Y V A A H S L W S E A K

2701 AACACAACCTGGAGCTGGTAGGTTGAATTAAGTTGATGCATGTGATGATTTATGTAGCT 2760
N N N L E L

2761 AGATCGAGCTAGCTATAATTAGGAGCATATCAGGTGCTGCTGACAACACCAGCCATACCA 2820
V L L T T P A I P

2821 GAAGACAGGATGAAGGAGATCACCAAGGCTTCAGAAGGCTTCGCTCTACCTGGTAGTTATA 2880
E D R M K E I T K A S E G F V Y L

2881 TGTATATATAGATGGACGACGTAACCTCATTCCAGCCCCATGCATATATGGAGGCTTCAAT 2940
2941 TCTGCAGAGACGACGAAGACCACGACGACTAACACTAGCTAGGGGCGTACGTTGCAG 3000

3001 GTGAGCGTGAACGGAGTGACAGGTCTCGCGCAAACGTGAACCCACGAGTGGAGTCACTC 3060
V S V N G V T G P R A N V N P R V E S L

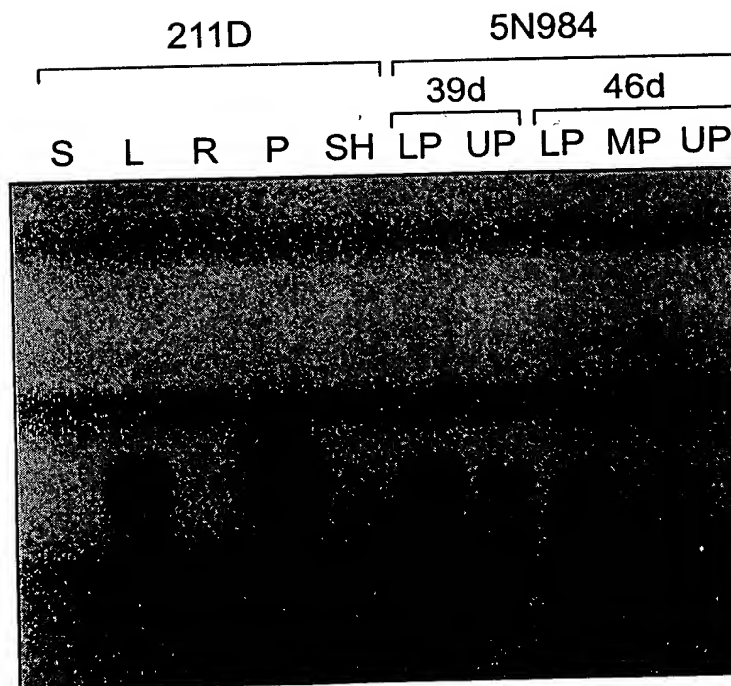
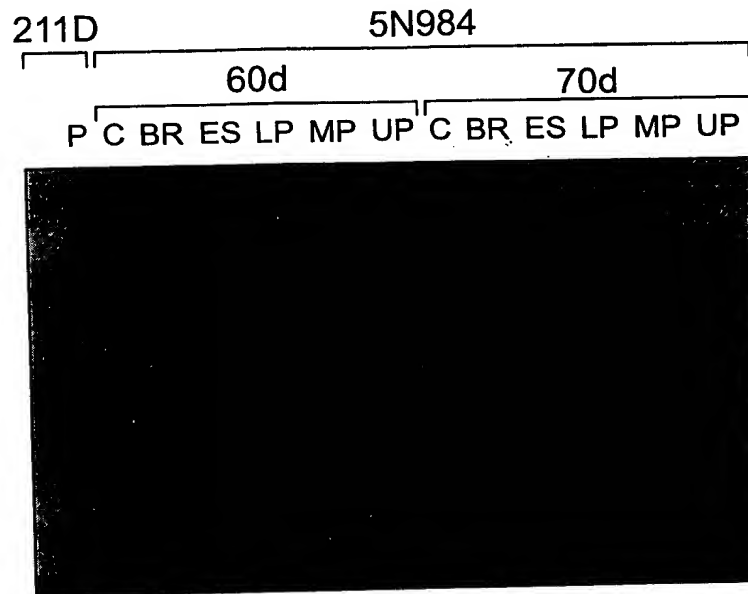
09983462 112001

Fig. 24C

3061 ATCCAGGAGGTTAAGAAGGTGACTAACAAGCCCGTTGCTGTTGGCTTCGGCATATCCAAG 3120
 I Q E V K K V T N K P V A V G F G I S K
 3121 CCCGAGCACGTGAAGCAGGTACGTACGTAGCTGACCAAAAAAACTGTTAACAAGTTTTG 3180
 P E H V K
 3181 TTTGACAAGCCGGCTACTAGCTAGCTAACAGTGATCAGTGACACACACACACACAGAT 3240
 Q I
 3241 TGCGCAGTGGGGCGCTGACGGGGTGATCATCGGCAGCGCCATGGTGAGGCAGCTGGGCGA 3300
 A Q W G A D G V I I G S A M V R Q L G E
 3301 AGCGGCTTCTCCCAAGCAAGGCCTGAGGAGGCTGGAGGAGTATGCCAGGGGCATGAAGAA 3360
 A A S P K Q G L R R L E E Y A R G M K N
 +++
 3361 CGCGCTGCCATGAGTCCATGACAAAGTAAAACGTACAGAGACACTTGATAATATCTATCT 3420
 A L P
 3421 ATCATCTCGGAGAAGACGACCGACCAATAAAAAATAAGCCAAGTGGAAGTGAAGCTTAGCT 3480
 3481 GTATATACACCGTACGTCGTCGTCGTTCCGGATCGATCTCGGCCGGCTAGCTAGCAG 3540
 3541 AACGTGTACGTAGTAGTATGTAATGCATGGAGTGTGGAGCTACTAGCTAGCTGGCCGTT 3600
 3601 ATTCGATTATAATTCTTCGCTCTGCTGTGGTAGCAGATGTACCTAGTCGATCTTGTACGA 3660
 3661 CGAAGAAGCTGGCTAGCTAGCCGTCTCGATCGTATATGTACTGATTAATCTGCAGATTGA 3720
 \$
 3721 ATAAAAACTACAGTACGCATATGATGCGTACGTACGTGTGTATAGTTTGTGCTCATATAT 3780
 3781 GCTCCTCATCACCTGCCTGATCTGCCCATCGATCTCTCTCGTACTCCTTCCTGTAAATG 3840
 3841 CCTTCTTTGACAGACACACCACCAGCAGTACGCTCTGCACGCCGCCGCTTAA 3900
 3901 GACATGTAAGATATTTTAAGAGGTATAAGATACCAAGGAGCACAAATCTGGAGCACTGGG 3960
 3961 ATATTGCAAAGACAAAAAACAATAAAGTCCCACCAAGTAGAGATAGTAAAGA 4020
 4021 GGTGGATGGATTAAATATCTCATGATTTTTGGATCTGCTCAAATAGATCGATATGGTA 4080
 4081 TTCAGATCTATGTTGTATAGCCTTTTCATTAGCTTTCTGAAAAAATGGTATGATGAG 4140
 4141 TGCGGAGTAGCTAGGGCTGTGAAGGAGTCGGATGGGCTTCCACGTACTTGTGTGGGCC 4200
 4201 TAGTCCGGTTCTATTTAGGTCCGATCCGAGTCCGGCATGGTCCGGTTCATACGGGCTAG 4260
 4261 GACCAAGCTCGGCACGTGAGTTTTAGGCCCGTCGGCTAGCCCGAGCACGCCGTTTTTA 4320
 4321 AACTGGCTAGGACTCGCCCATTTAATAAGACAAACATTGCAAAAAATAGCTCTATTTTTT 4380
 4381 ATTTAAAATATATTGTTTATTGTGAAATGTGTATTATTTGTAATATATATTATTGTATA 4440
 4441 TAGTTATATCTTCAATTATGATTTATAAATATGTTTTTTATTATGAACCAATTTTAAGT 4500
 4501 TTGATTTATGCGTTGGCGGGCTCGAGGAGGCACGGTGAACATTTTTGGGTCGGGCTTAAC 4560
 4561 GGGTCGGCCCGGCCCGGTTCCGGCCCATCCACGGCCCATCCCGTGTGCGCCTCGTTCGGTG 4620
 4621 AGTTCAGCCCGTCGGACAACCCGTCCCCGGCCGATAATTAATCGGGCCTAACCGTGCG 4680
 4681 GTGCTTAAACGGTCCGTGCCTCAACGACCGGGCGGGCGGCCCGTTTGACATCTCTA 4740
 4741 GTGGTGTGATTAGAGATGGCGATGGGAACCGATCACTGATTCCGTGTGGAGAATTTCGATA 4800
 4801 TCAAGCTTATCGATACC 4817

Entire sequence of the maize TrpA gene, with introns and exons, transcription and translation strats, start and stop of cDNA.
 \$ = start and end of cDNA; +1 = transcription start; 73***** = primer extension primer; ▼ = start of translation; +++ = stop codon; = CCAAT Box, TATAA Box, poly A addition site.
 # above underlined sequences are PCR primers.

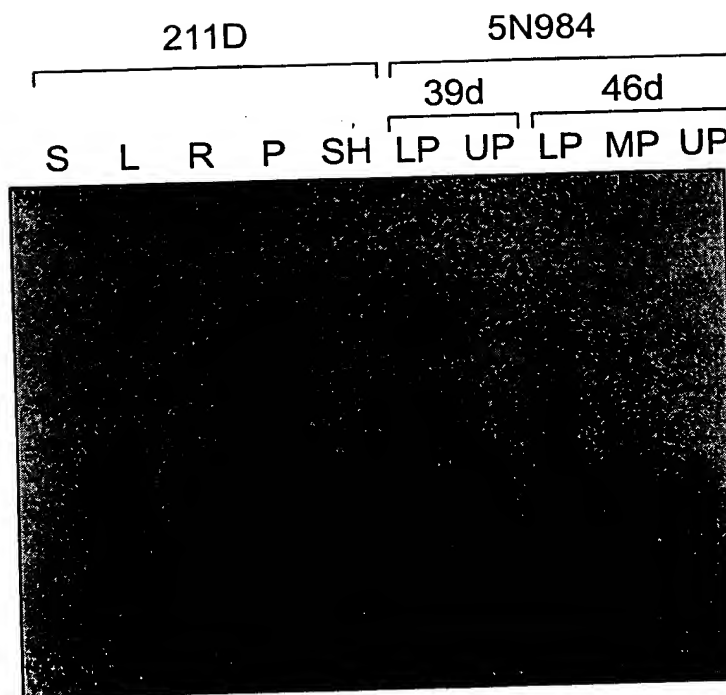
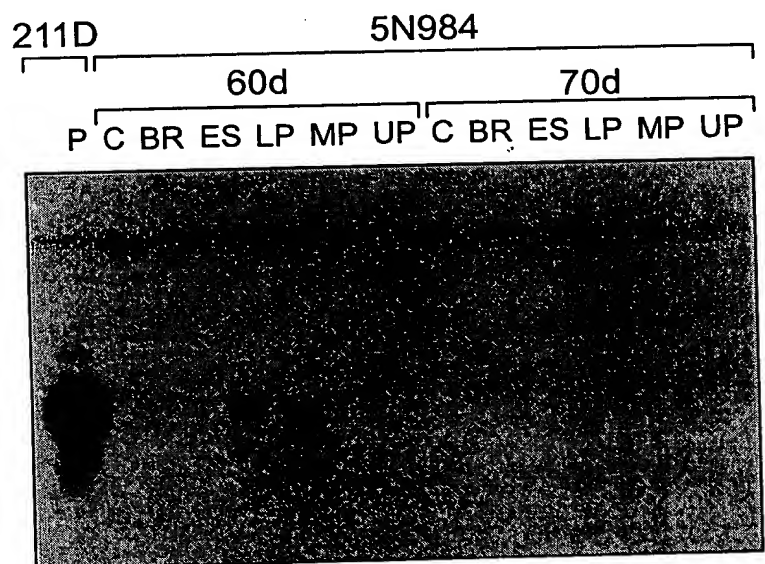
094421 29483660



Northern blot showing differential expression of TrpA gene in maize tissues. 2 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25A

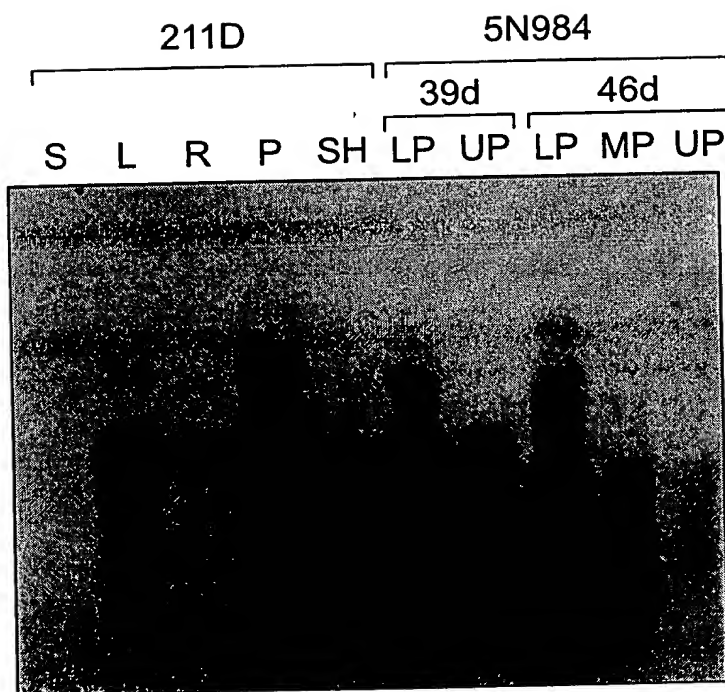
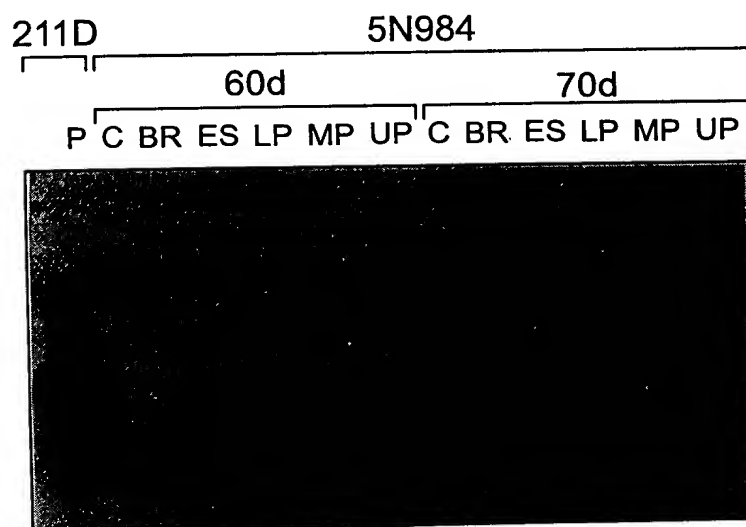
0993462-112001



Northern blot showing differential expression of TrpA gene in maize tissues. 4 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25B

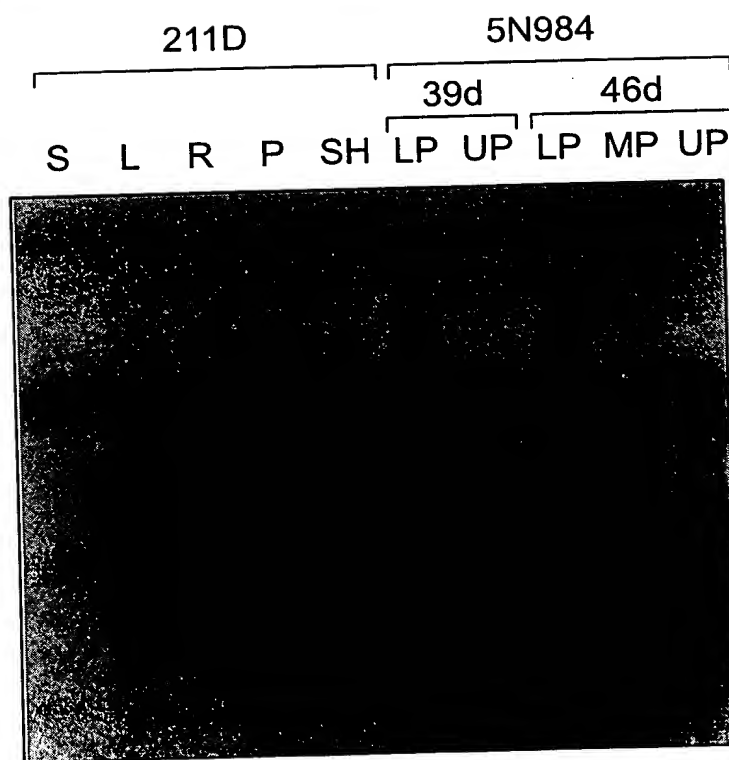
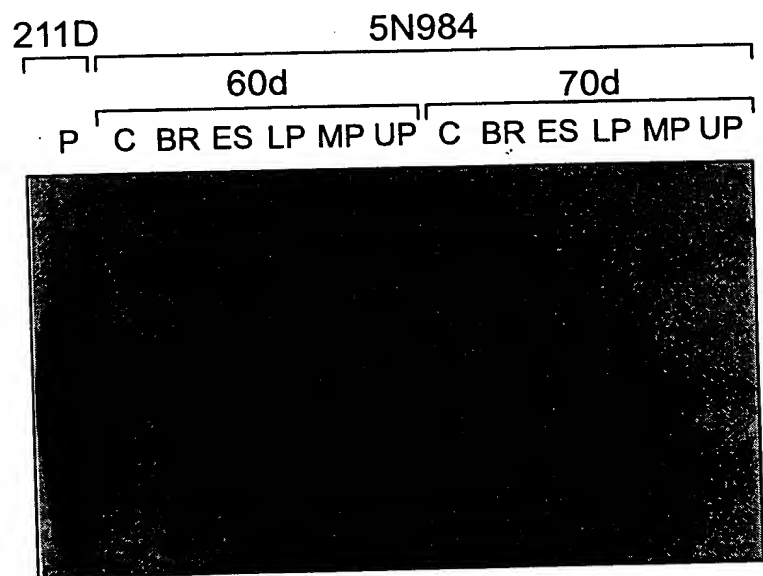
000217 2948660



Northern blot showing differential expression of TrpA gene in maize tissues. 18 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25C

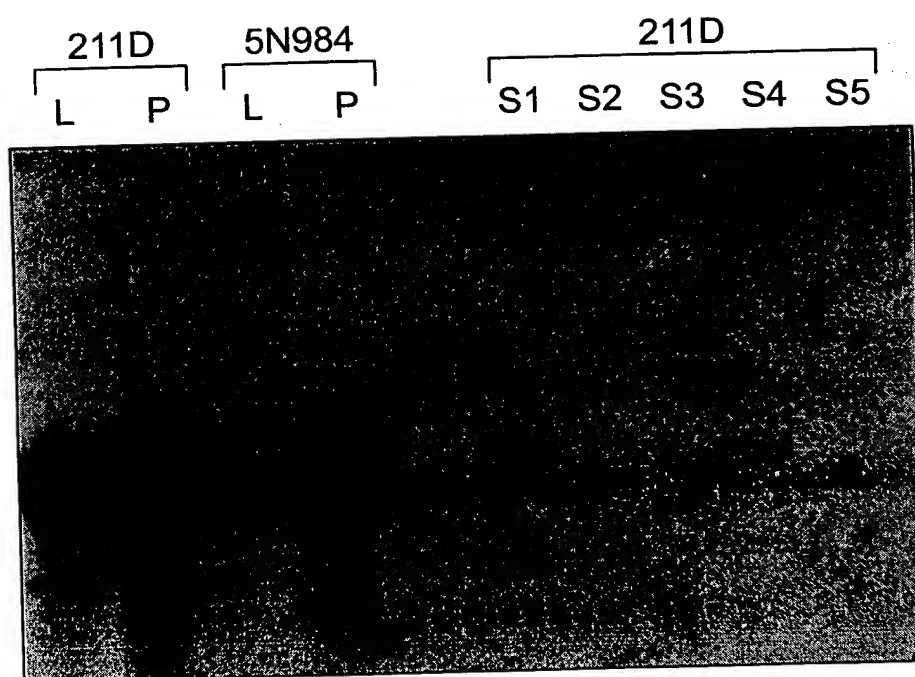
096346-12001



Northern blot showing differential expression of TrpA gene in maize tissues. 48 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25D

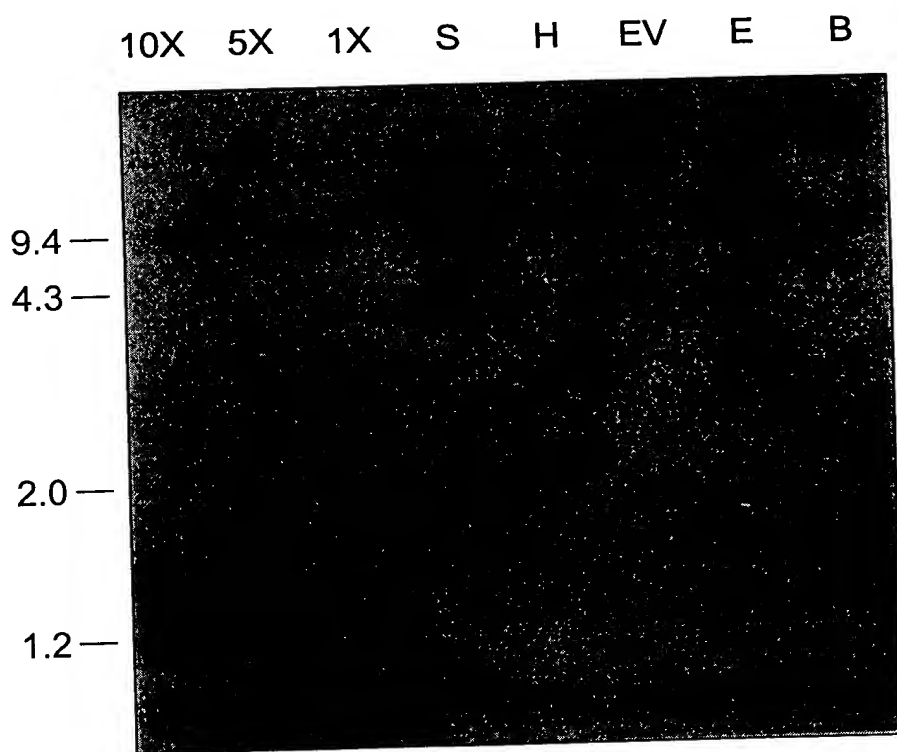
0998452-112001
"29488660"



Northern blot showing maize TrpA gene expression in Funk lines 211D and 5N984 leaf and pith and the absence of expression in 211D seed total RNA. 65 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 26

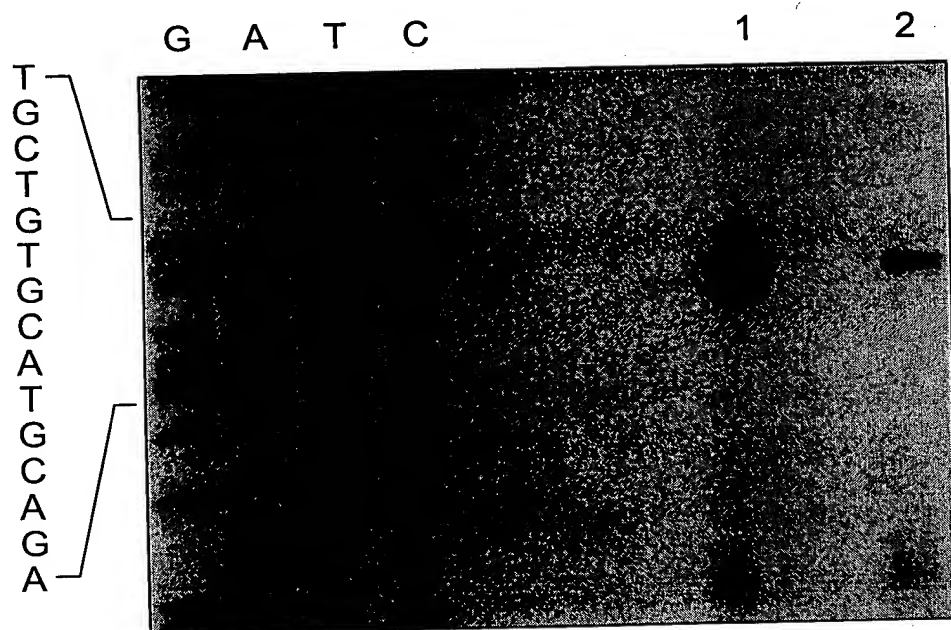
0908462-112001



Genomic southern of Funk line 211D probed with the TrpA cDNA 8-2. B = BamHI, E = EcoRI, EV = EcoRV, H = HindIII and S = SacI. 120 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 27

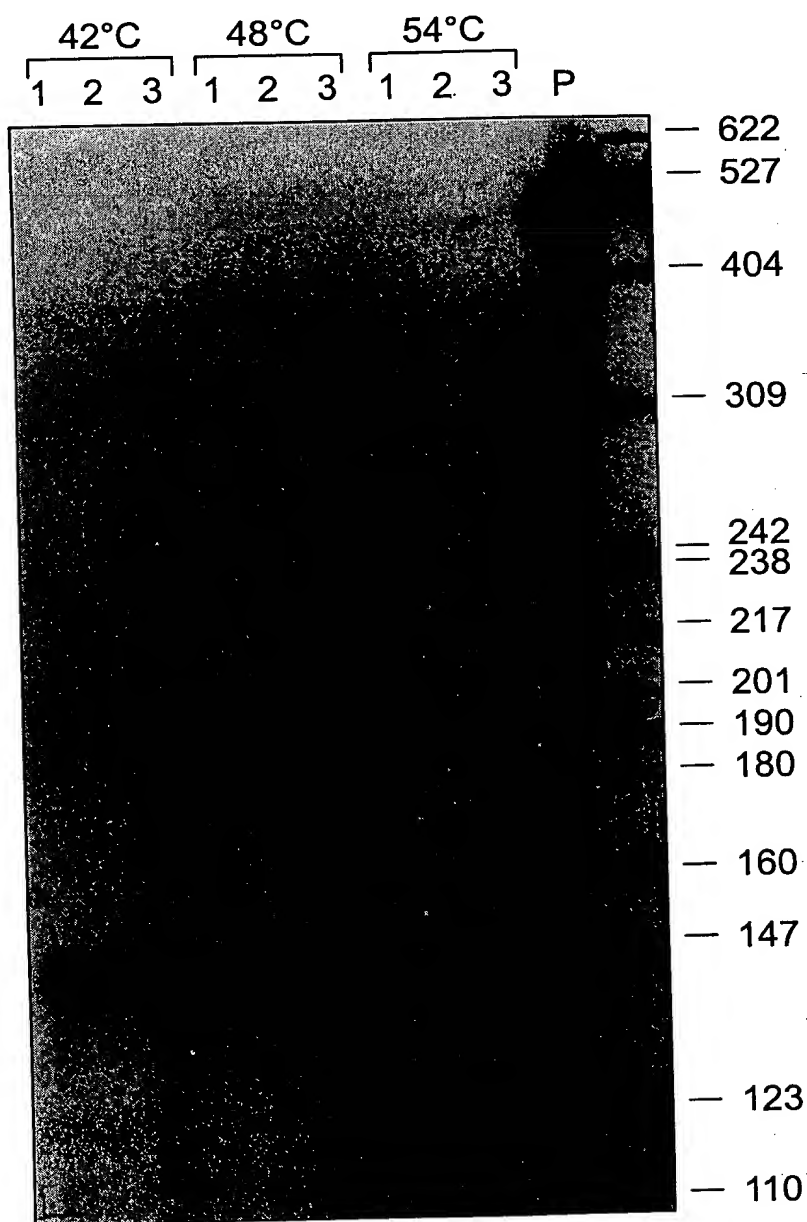
09983462.112001



Primer extension showing the transcription start of TrpA gene and sequencing ladder.
1 hour exposure against film at -80C with Dupont Cronex intensifying screens.

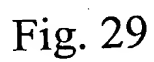
Fig. 28A

090846-12001
100271-29488660



RNase protection of region from +2 bp to +387 bp
with three annealing temperatures.
16 hour exposure against film at -80C with Dupont Cronex
intensifying screens.

Fig. 28B



TOTAL OF \$60,987

①

Fig. 30A

Maize Pollen CDPK cDNA sequence
sequence contained in clones pCIB3168 and pCIB3169

1 TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC CGC GGC GCG
119 Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala

57 TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG TGC GCG GGC GGG GAG CTC
191 Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly Gly Glu Leu

Aval
114 TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC ACG GAG CGC GGC GCC GCG GAG CTG CTG
38 Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg Gly Ala Ala Glu Leu Leu

171 CGC GCC ATC GTG CAG ATC GTG CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC
57 Arg Ala Ile Val Gln Ile Val His Thr Cys His Ser Met Gly Val Met His Arg Asp

Aval
228 ATC AAG CCC GAG AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC
76 Ile Lys Pro Glu Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala

285 ACC GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC ATC GTC
95 Thr Asp Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val

Aval
342 GGC AGC GCC TAC TAC ATC GCG CCC GAG GTG CTC AAG AGG AAG TAC GGC CCG GAG GCC
114 Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro Glu Ala

399 GAC ATC TGG AGC GTC GGC GTC ATG CTC TAC ATC TTC CTC GCC GGC GTG CCT CCC TTC
133 Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala Gly Val Pro Pro Phe

456 TGG GCA GAG AAC GAG AAC GGC ATC TTC ACC GCC ATC CTG CGA GGC CAG CTT GAC CTC
152 Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu

513 TCC AGC GAG CCA TGG CCA CAC ATC TCG CCG GGA GCC AAG GAT CTC GTC AAG AAG ATG
171 Ser Ser Glu Pro Trp Pro His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met

570 CTC AAC ATC AAC CCC AAG GAG CGG CTC ACG GCG TTC CAG GTC CTC AAT CAC CCA TGG
190 Leu Asn Ile Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp

627 ATC AAA GAA GAC GGA GAC GCG CCT GAC ACG CCG CTT GAC AAC GTT GTT CTC GAC AGG
209 Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp Arg

684 CTC AAG CAG TTC AGG GCC ATG AAC CAG TTC AAG AAA GCA GCA TTG AGG ATC ATA GCT
228 Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu Arg Ile Ile Ala

741 GGG TGC CTA TCC GAA GAG GAG ATC ACA GGG CTG AAG GAG ATG TTC AAG AAC ATT GAC
247 Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys Glu Met Phe Lys Asn Ile Asp

798 AAG GAT AAC AGC GGG ACC ATT ACC CTC GAC GAG CTC AAA CAC GGC TTG GCA AAG CAC
266 Lys Asp Asn Ser Gly Thr Ile Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His

855 GGG CCC AAG CTG TCA GAC AGC GAA ATG GAG AAA CTA ATG GAA GCA GCT GAC GCT GAC
285 Gly Pro Lys Leu Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp

EcoRI
912 GGC AAC GGG TTA ATT GAC TAC GAC GAA TTC GTC ACC GCA ACA GTG CAT ATG AAC AAA
304 Gly Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys

09988452 "112001

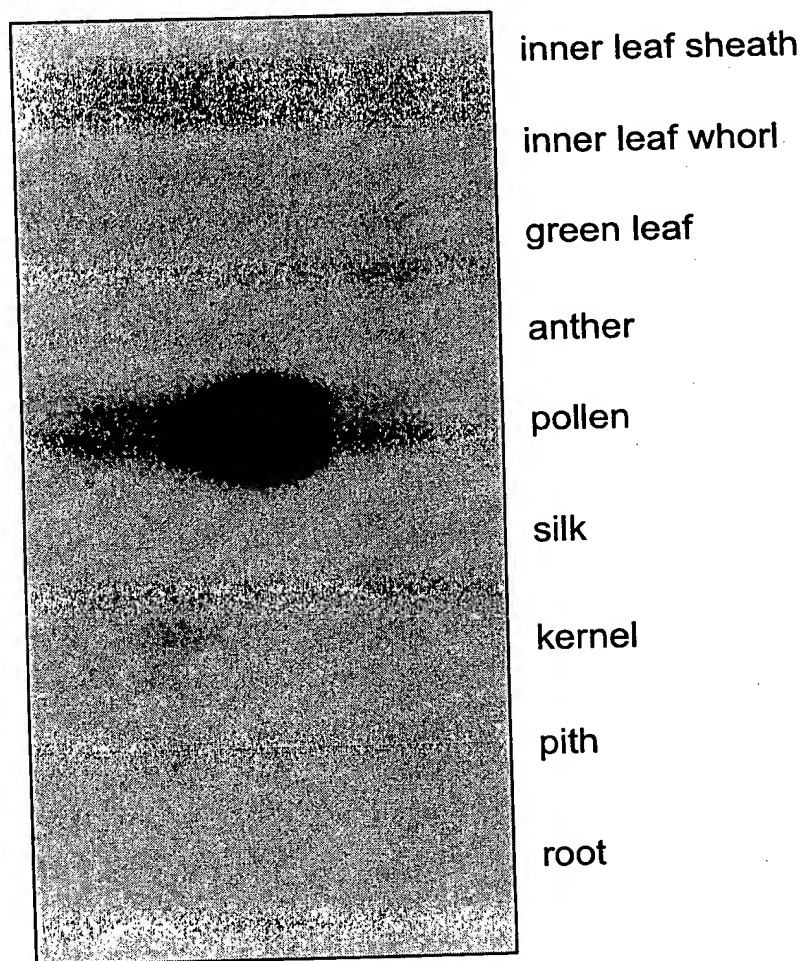


Fig. 31

096462 **J. 2081**

Lipman-Pearson Protein Alignment
Gap Penalty: 2; Gap Length Penalty: 12

Seq1	Seq2	Similarity	Gap	Gap	Consensus
pol CDPK ptn	rat pk2 ptn	Index	Number	Length	Length
1>551	1>528	36.5	4	4	297

pol CDPK ptn YSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDDVDRREVQIMHHLSGQPNVVGLRGAYE 162
Y : .ELG:G.F:V.: C.:TS.:. A K.I.:KL:AR:: :. RE.:I : L. :PN:V L::.
rat pk2 ptn YQLFEELGKGAFSVVRRCKKTSTQEYAAKIINTKKLSARDH-QKLEREARICRLK-HPNIVRLHDSIS 81

pol CDPK ptn DKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTCHSMGVMHRDIKPENFLLLSKDEDA 232
 .. .LV...:GGELF: I:AR. Y:E :A:::I:: V: H ::HRD:KPEN:LL SK :A
 rat pk2 ptn EEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILESNNHIIHQHDIVHRDLKPENLLLASKCKGA 151

pol CDPK ptn PLKATDFGLSVFFK-EGELLRDIVGSAYYIAPEVL-KRKYGPEADIWSVGVMLYIFLAGVPPFFWAENENG 300
::K :DFGL:: : : : :G:: Y::PEVL:: YG .DIW: GV:LYI:L.G PPFW.E:::
rat pk2 ptn AVKLA DFGLAIEVQGEQQAWFGFAGTPGYLSPEVLRKDPYGPVDIWACGVILYILLVGYPFFWDEDQHK 221

```
pol CDPK ptn IFTAILRGQLDLSSEPWPWHISPGAKDLVKMMLNINPKERLTAFOVLNHPWIKEDGDAPDTPLDNVVLDR L 370  
:: .I G. D : S W :: P.A.K:L:: ML.INP .R:TA Q.L:HPW: : : : : : : : : : L  
rat pk2 ptn LYQQIKAGAYDFPSPEWDVTPEAKNLINQMLTINPAKRITADQALKHPWCQRSTVASMMHRQETVECL 291
```

pol CDPK ptn KQFRAMNQFKKAALRII 387
::F.A...:K A L ::
rat pk2 ptn RKFNARRKLKGAILTMM 308

Fig. 33

Lipman-Pearson Protein Alignment

Gap Penalty: 2; Gap Length Penalty: 12

Seq1	Seq2	Similarity	Gap	Gap	Consensus
pol CDPK ptn	humcama ptn	Index	Number	Length	Length
1>551	1>150	40.3	2	2	142

pol CDPK ptn LSEEEITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKLSDSEMEKLMEAADADGNGLIDYDEFVTATV 460
 L:EE:I::KE F. :DKD..GTIT .EL : . G.: ::E:::.....DADGNG ID: EF:T .
 humcama ptn LTEEQIAEFKEAFSLFDKGDGTITTKELGTVMRSLGQNPTAELODMINEVDADGNGTIDFPEFLTMA 74

pol CDPK ptn HMNKL-DREEHLYTAFQYFDKDNSGYITKEELEHALKEQGLYDADKIKDI-ISDADSDNDGRIDYSEFVA 528
 : M:. D.EE:: .AF: FDKD.:GYI: .EL H.: : GI.:AD D.DG:::Y.EFV.
 humcama ptn RKMKDTDSEEEIREAFRVKDKGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGGQVNYEEFVQ 144

pol CDPK ptn MM 530
 MM
 humcama ptn MM 146

0000462.12001
 T002T"2948860

2025 年 1 月 1 日

Gap Penalty: 2; Gap Length Penalty: 12

pol CDPK ptn	VLGRPMEDVRATYSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDDVDDVRREVQIMHHLSG	150
soybean CDPK ptn	VLPQRTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRKLLCKEDYEDVWREIQIMHHLSE	91
pol CDPK ptn	QPNVVGLRGAYEDKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTCHSMGVMHRDIKP	220
soybean CDPK ptn	HANVVRIEGTYEDSTAVHLVMELCAGGELFDRIVQKGHYSERQAARLIKTIVEVVEACHSLGVMHRDLKP	161
pol CDPK ptn	ENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIAPEVLKRKYGPEADIWSVGVMLYIFLAGV	290
soybean CDPK ptn	ENFLFDTIDEDAKLKATDFGLSVFYKPGESFCDVVGSPPYYVAPEVLRKLYGPESDVWSAGVILYILLSGV	231
pol CDPK ptn	PPFWAENENGIFTAILRGQLDLSSEPWPHPISPGAKDLVKKMLNINPKERLTAFQVLNHPWIKEDGDAPDT	360
soybean CDPK	PPFWAESEPGIFRQILLGKLDHFHSEPWPSPISDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDK	301
pol CDPK ptn	PLDNVVLDRLKQFRAMNQFKKAALRIIAGCLSEEEITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKL	430
soybean CDPK ptn	PLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTNSGTITFDELKDGLKRVGSEL	371
pol CDPK ptn	SDSEMEKLMEAADADGNGLIDYDEFVTATVHMNKLDREEHLYTAFQYFDKDNSGYITKEELEHALKEQGL	500
soybean CDPK ptn	MESEIKDLMDAADIDKSGTIDYGEFTAATVHLNKLEREENLVSAFSYFDKDGSGYITLDEIQACKDFGL	441
pol CDPK ptn	YDADKIKDIISDADSNDGRIDYSEFVAMMRKGTAGAEPNIIK	544
soybean CDPK ptn	-DDIHIDMIKEIDQDNDGQIDYGEFAAMMRKGNNGIGRRTMRK	484

Fig. 35A

pol CDPK gene Map (1 > 4165)

Site and Sequence

Enzymes : 6 of 198 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

TTAGTAACACCTCTCCAATCGCTTGGGTTGGCACATTCTTAGCTTTATCACATTTTAAGAAATAGAGTTCACCACCTTC 80

AAAATATGCCTATACAATGAATGATGCTTGGATGCAATATAGCTAGATTCAACTAGCTATATATGGTCAATAGAACCCTG 160

TGAGCACCTCACAACACGACTTCAATTTTGAGACCCTAAGCGAGTAAATGGTTAAAGTCCTCTTATTATTAGTCTTAGG 240

ACTTCTCCTTGCTAAATGCTTGTGACGATCTATATATCTTCCCCACTGCGGGAGATACTATATATAGGGCCTTGGACCT 320

CTAGGGTATCTCAAAGGCCTAGTCACAACAATTCTCAACAGTATTTAATTTTATACATGTATGAACAGTGTAGGAATTTG 400

AGTGCCCAACCAAGAGTGGGAGGTGTAAATTGGGTAGCTAAACTTAAATAGGGCTCTTCTTATTTAGGTTTATCTAGTC 480

TCTACTTAGACTAATTCAGAAAGAATTTTACAACCTATGGTTAATCATATCTCTAGTCTAAGCAAATTTAGGAAAGTTAA 560

AAGCACACAATTAGGCACATGTGAAAGATGTGTATGGTAAGTAAAGACTTATAAGGAAAAAGTGGGTGAATCCTCAAGA 640

TGTGGTGGTATATCCAATGATATTAGATGCCAGAATATAGGGGGGAAATCGATGTATACCATCTCTACCAGGATACCTG 720

TGCGGACTGTGCAACTGACACATGGACCATGGTGTCTTCTTAGATTTGGTTATTAGCTAATTGCGCTACAACCTGTTCAA 800

GGCTAGACCAAATTAATAAACTAATATTAACATAAAAAGTTAGGCAAACCTATAGTAAATTATGCAGCGATCCAACAACA 880

AGCCATGTCTCGTGGGTCATGAGCCACGCGTCGGCCATACACCCACATGATGTTTCCATACGGATGGTCCTTATGCAATT 960

TTGTCTGCAAAACACAAGCCTTAATACAGCCACGCGACAATCATGGAAGTGGTCGTTTTAGGTCCTCATCATGAAGTTCA 1040

GGGAAAACGCATCAAATGTAATGCAGAGAAATGGTATTTCTTCTCTTGTAATCAGGGAGAGGAGTACCATCAGTACAGA 1120

EcoRI

TTCAGAATCAGAATTCAGTCTTCCAACGACAATAATCGCAGCATCTGTAAAAATTGCAGAACTTCTGTTTGACTTGT 1200

AGCCCTGACCTTTGCAAATATTTGAAGTTGTGCCTGCTGACACAACCTCAATCTGGAAGTGCTGTTGATCAGTTTTGCCA 1280

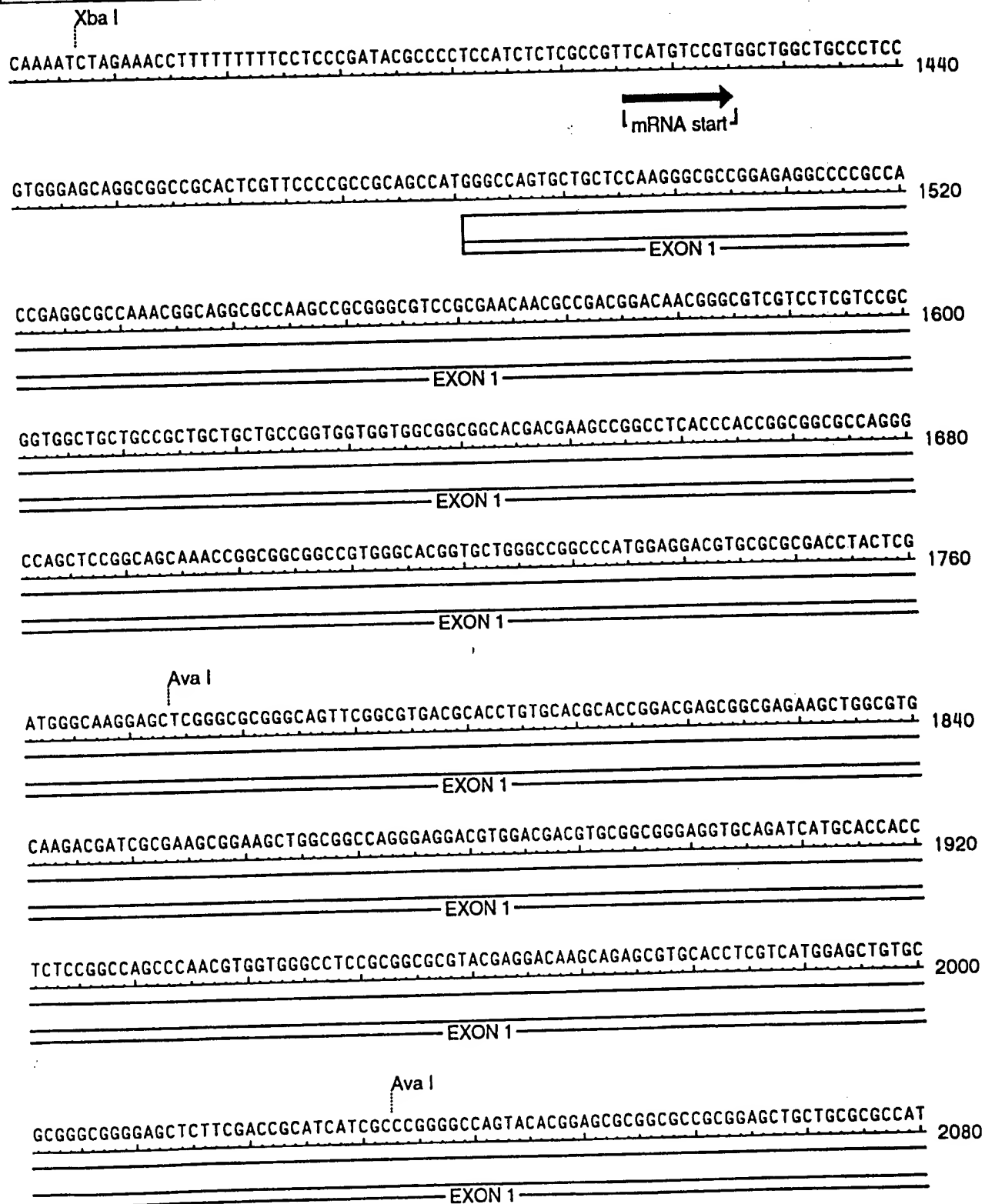
GAAACAGCAAGCAGCCTATATATATCTGTACGAGACACCCTGCCGCCCTCTTCTTTCCCGCCATTCCCTCCCTACCCTT 1360

09988462-112001

Fig. 35B

pol CDPK gene Map (1 > 4165)

Site and Sequence



09988462.1.12001

Fig. 35C

pol CDPK gene Map (1 > 4165)

Site and Sequence

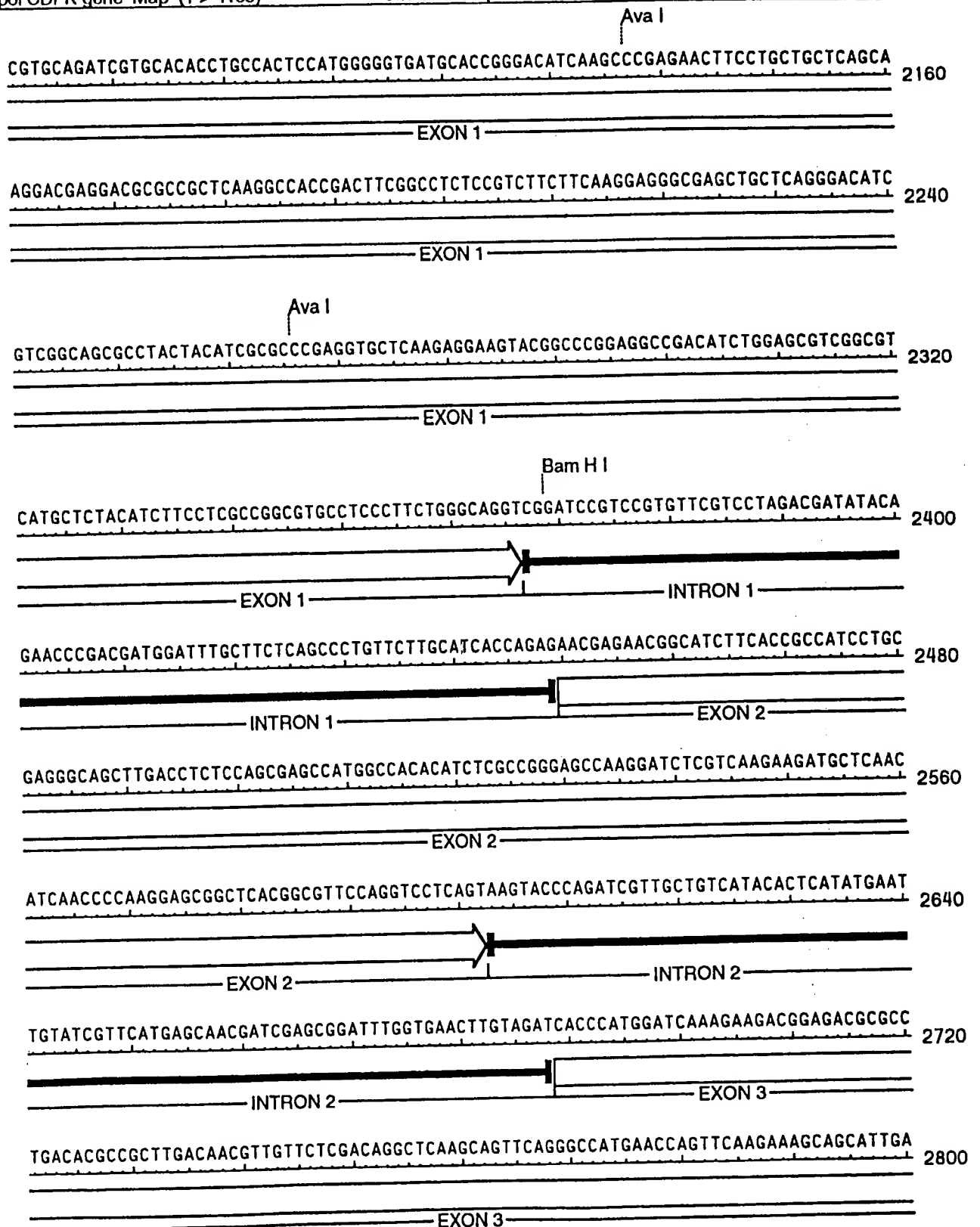


Fig. 35D

pol CDPK gene Map (1 > 4165)

Site and Sequence

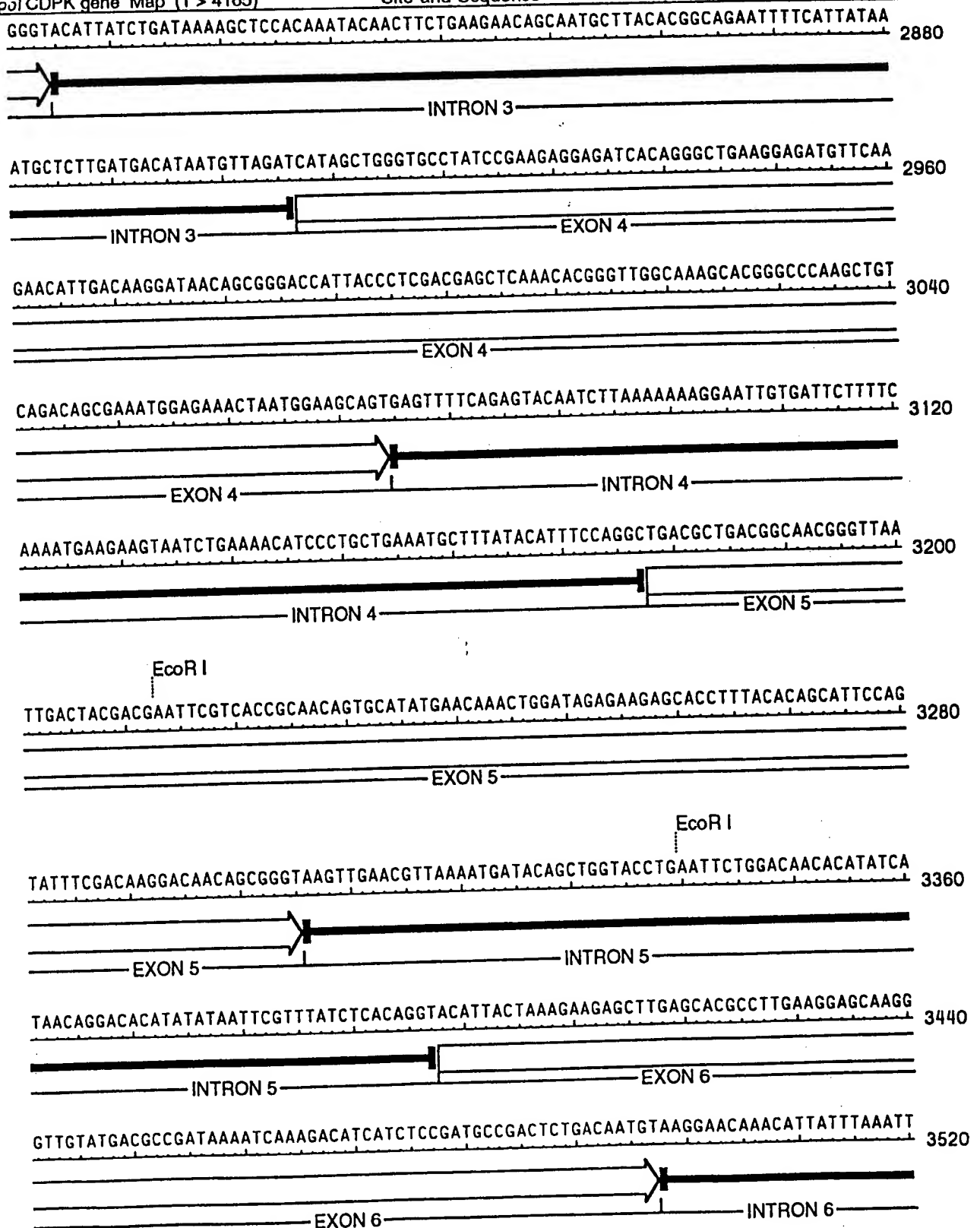
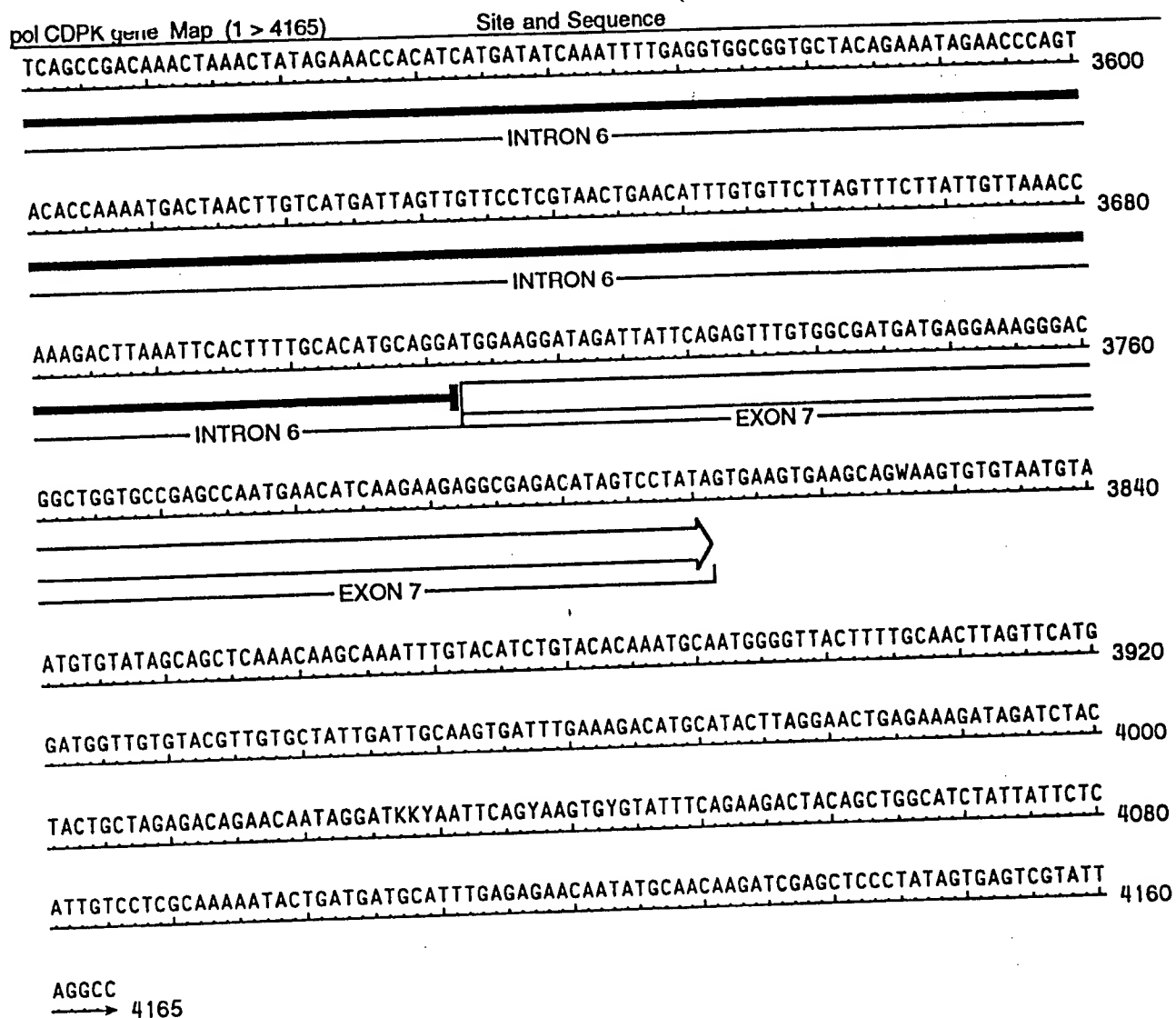


Fig. 35E



09988462.112001

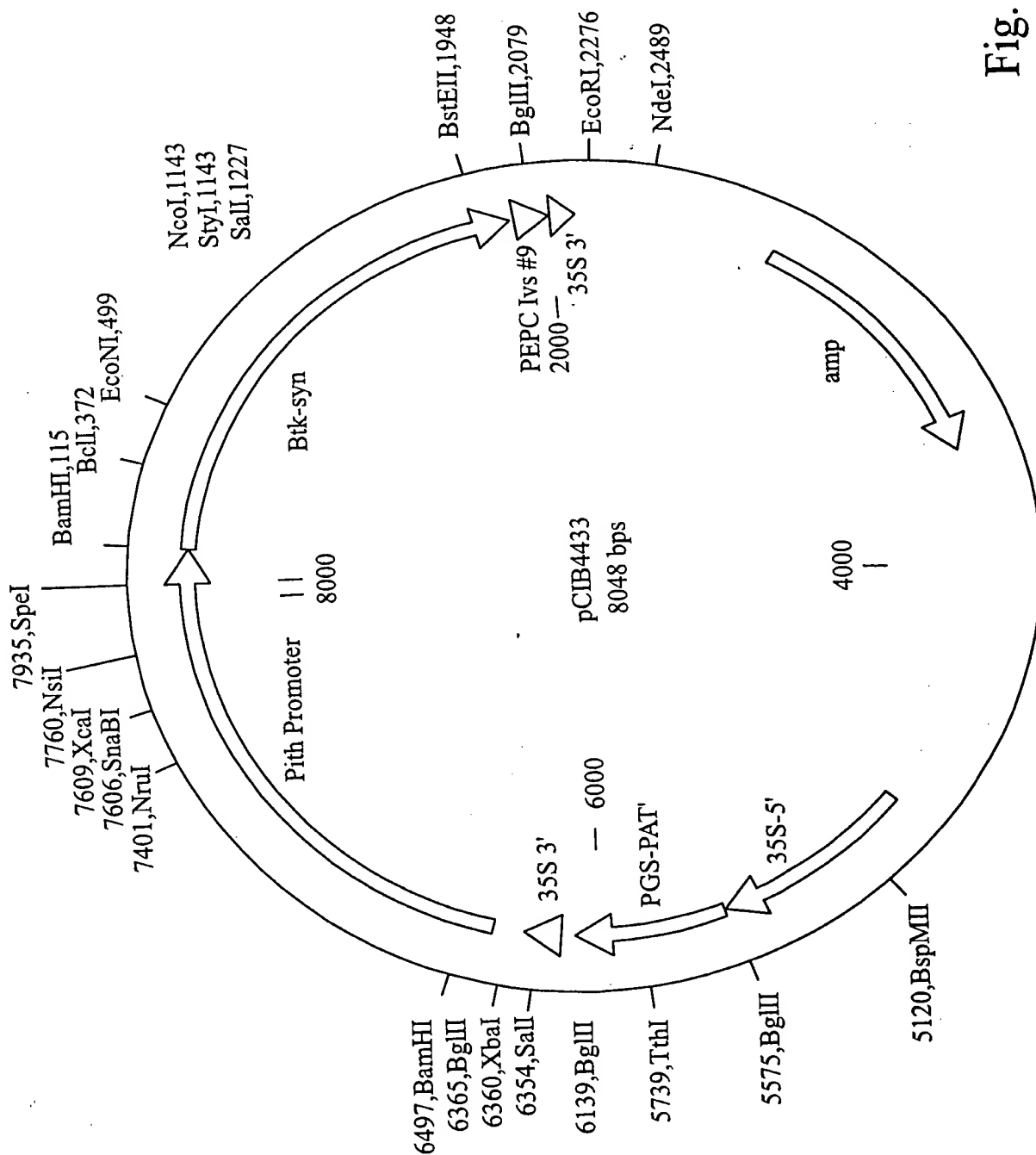


Fig. 36

Fig. 37A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
NetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG
ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTGGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCTG
GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG
LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCCTG
LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCCGTGCG CTTACGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

09088462 "112004

Fig. 37B

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA CCATGTTCCG CAGTGGCTTC
ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACACCA ACCTGCAGTT CCACACCAGC
GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT
ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

2041 CGGAATTTAC TTCAAGATCC AAACCTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 TTAGAAATCT ATTTAATTCT CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGAA AATGTGGGGA GCCGAATCGA
GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCATC ATTCCCATCA TTTCTCCTTG GACATTGATG TTGGATGTAC AGACTTAAAT
CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACTTAG GTGTATGGGT GATATTCAAG ATTAAGACGC AAGATGGCCA TGCAAGACTA
GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGAAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

09988462 112001

Fig. 37C

2641 AGAGCGGAGA 2VGWkTGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCTGA
GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

3061 GTTCGTGTCT GTCCGGGTCTG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAAATGA TTATACTGCG
AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAATAA
Glu---

09983462-112001

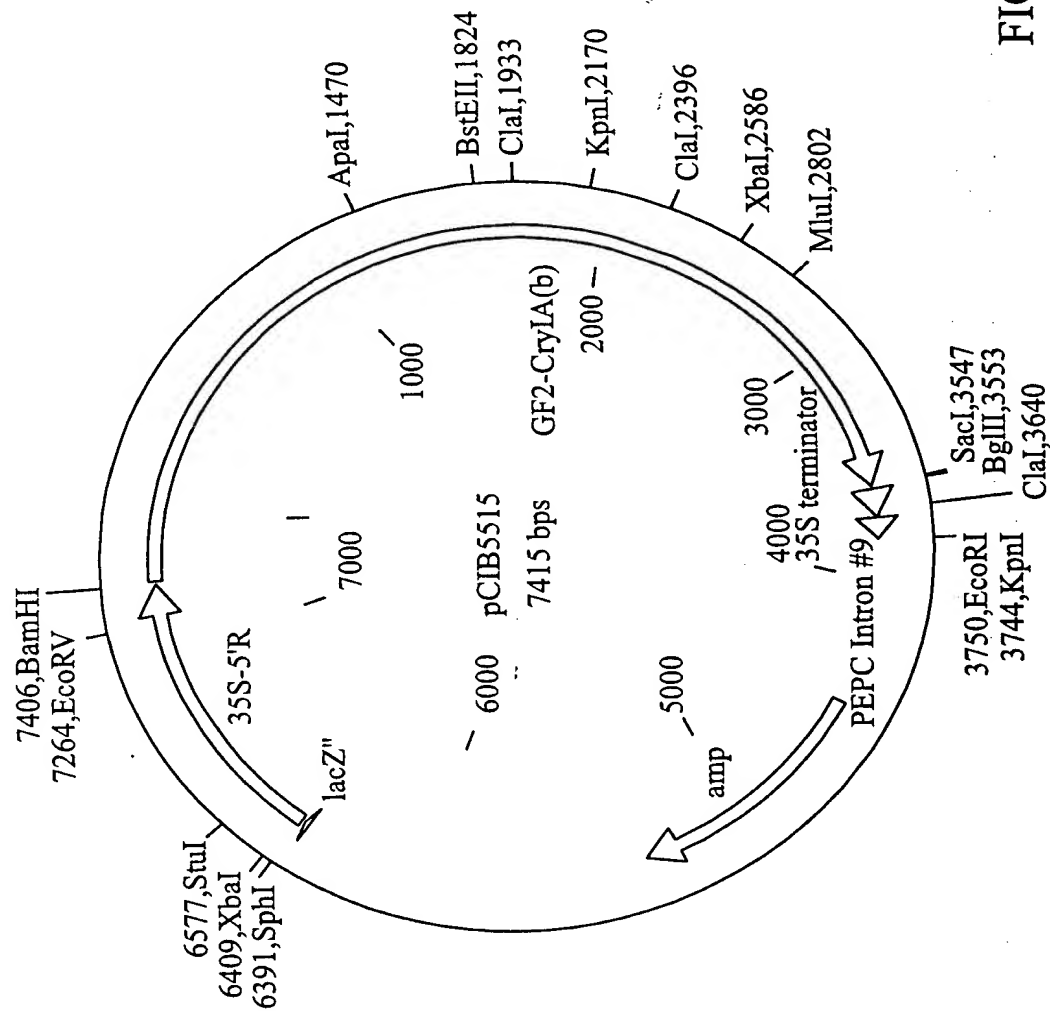


FIG. 38